

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 23, 2005, 01:47:14 ; Search time 77 Seconds
(without alignments)
372.421 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 BACNLPYVRGPCIAPFPFRA.....QGNKMKYSEKREYGV 56

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	296	90.0	151	2 P78491	P78491 homo sapien
2	296	90.0	352	1 AMBP_HUMAN	P02760 homo sapien
3	272	82.7	337	1 AMBP_PIG	P04366 sus scrofa
4	269	80.8	352	1 AMBP_BOVIN	P00878 bos taurus
5	264	81.2	125	1 IATR_HORSE	P04365 equus caball
6	261	79.3	349	1 AMBP_MOUSE	Q07456 mus musculus
7	261	79.3	349	2 Q925W1	Q925W1 mus musculus
8	261	79.3	349	2 Q9DBJ9	Q9DBJ9 mus musculus
9	259	78.7	346	1 AMBP_MERUN	Q62577 meriones un
10	258	78.4	349	1 AMBP_RAT	Q64240 rattus norv
11	257	78.1	123	1 IATR_CAPRI	P62756 capra hircu
12	257	78.1	123	1 IATR_SHEEP	P62757 ovis aries
13	254	77.2	349	1 AMBP_MESAU	Q60559 mesocricetu
14	253	76.9	352	2 Q70160	Q70160 cavia porce
15	232	70.5	342	2 Q6P2V8	Q6P2V8 xenopus tro
16	228	69.3	342	2 P70004	P70004 xenopus lae
17	228	69.3	342	2 Q7S246	Q7S246 xenopus lae
18	227	69.0	51	2 P78492	P78492 homo sapien
19	207	62.9	216	2 Q7SXH6	Q7SXH6 brachydantio
20	182	55.3	283	2 Q6ZNI4	Q6ZNI4 homo sapien
21	182	55.3	283	2 Q8TEU8	Q8TEU8 homo sapien
22	182	55.3	576	2 Q6UXZ9	Q6UXZ9 homo sapien
23	176	53.5	571	2 Q7TQX3	Q7TQX3 mus musculus
24	172	52.3	491	2 Q7LDM0	Q7LDM0 homo sapien
25	172	52.3	548	2 Q6GNZ8	Q6GNZ8 homo sapien
26	169	51.4	759	2 Q8IT91	Q8IT91 ancylostoma
27	165	50.2	107	2 Q8I007	Q8I007 drosophila
28	160	48.6	90	2 Q6T6T5	Q6T6T5 bits gabon
29	159	48.3	2419	2 Q7PEZ1	Q7PEZ1 anopheles g
30	157	47.7	133	2 Q8H245	Q8H245 papio papio
31	156	47.4	35	2 Q951C3	Q951C3 sus scrofa

32	156	47.4	90	2 Q6T6S5	Q6T6S5 bits gabon
33	155	47.1	111	2 Q7M4L3	Q7M4L3 homo sapien
34	155	47.1	523	2 Q14594	Q14594 homo sapien
35	155	47.1	751	2 Q60709	Q60709 mus musculus
36	155	47.1	763	1 APP2_HUMAN	Q06481 homo sapien
37	155	47.1	763	2 Q7IUI0	Q7IUI0 homo sapien
38	155	47.1	763	2 Q61482	Q61482 mus musculus
39	155	47.1	765	1 APP2_RAT	P15943 rattus norv
40	154	46.8	195	2 Q9DBQ8	Q9DBQ8 mus musculus
41	154	46.8	252	1 SPT2_MOUSE	Q9WU03 mus musculus
42	154	46.8	327	2 Q6IND9	Q6IND9 xenopus lae
43	153	46.5	76	2 CST1_BOVMO	P81902 bombyx mori
44	153	46.5	76	2 Q8T7I9	Q8T7I9 bombyx mori
45	152	46.2	122	1 BTA1_BOOMI	P83609 boophilus m

ALIGNMENTS

RESULT 1

P78491 PRELIMINARY; PRT; 151 AA.

AC P78491; 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-1-microglobulin (Bikunin) (Fragment).
GN Name=alpha-1-microglobulin-bikunin;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91214554; PubMed=1708673;
RA Vetr H., Gebhard W.,
RT "Structure of the human alpha-1-microglobulin-bikunin gene."
RL Biol. Chem. Hoppe-Seyler 371:1185-1196 (1990).
CC -I- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: X54818; CAN38587.1; -.
DR HSSP: P02760; IBIK.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot. Inh. Kunitz-m.
DR Pfam: PF00014; Kunitz BPTI; 2.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot. Inh. Kunitz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
FT NON TER 151 151
SQ SEQUENCE 151 AA; 16542 MW; 88F400C5E6CA19831 CRC64;
Query Match 90.0%; Score 296; DB 2; Length 151;
Best Local Similarity 92.7%; Pred. No. 3e-27;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ACNLPYVRGPCIAPFPFRAFDVKGKCVLPFGGCGQGNKMKYSEKREYGV 56
DB 85 ACNLPYVRGPCIAPFPFRAFDVKGKCVLPFGGCGQGNKMKYSEKREYGV 56
AMBP_HUMAN STANDARD; PRT; 352 AA.
ID AMBP_HUMAN
AC P02760; P00977; P02759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE AMBP protein precursor (Contains: Alpha-1-microglobulin (Protein HC)
(Complex-forming glycoprotein heterogeneous in charge) (Alpha-1-microglobulin); Inter-alpha-trypsin inhibitor light chain (ITI-LC)
(Bikunin) (HI-30)).
DE Name=AMBP; Synonyms=HCP, ITIL;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91214554; PubMed=1708673;
RA Vetr H., Gebhard W.;
RT "Structure of the human alpha 1-microglobulin-bikunin gene.";
RL Biol. Chem. Hoppe-Seyler 371:1185-1196(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=87040757; PubMed=2430261;
RA Kaumeyer J.F., Polazzi J.O., Kotlick M.P.;
RT "The mRNA for a proteinase inhibitor related to the HT-30 domain of
inter-alpha-trypsin inhibitor also encodes alpha-1-microglobulin
(protein HC).";
RL Nucleic Acids Res. 14:7839-7850(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90336621; PubMed=1696200;
RA Diarra-Nehpou M., Bourguignon J., Sessboue R., Salier J.-P.,
Leveillard T., Martin J.P.;
RT "Structural analysis of the human inter-alpha-trypsin inhibitor light-
chain gene.";
RL Eur. J. Biochem. 191:131-139(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
Diacchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Miliady S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton B., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-220 FROM N.A.
RX MEDLINE=86312901; PubMed=2428011;
RA Traboni C., Cortese R.;
RT "Sequence of a full length cDNA coding for human protein HC (alpha 1
microglobulin).";
RL Nucleic Acids Res. 14:6340-6340(1986).
RN [6]
RP SEQUENCE OF 20-202.
RX MEDLINE=84126849; PubMed=618962;
RA Lopez C., Grubb A.O., Mendez E.;
RT "The complete amino acid sequence of human complex-forming
glycoprotein heterogeneous in charge (protein HC) from one
individual.";
RL Arch. Biochem. Biophys. 228:544-554(1984).
RN [7]
RP SEQUENCE OF 20-198.
RX MEDLINE=9332026; PubMed=768253;
RA Enghild J.J., Salvesen G., Thøgersen I.B., Valnickova Z., Pizzo S.V.,
Hefza S.A.;
RT "Human protein HC displays variability in its carboxyl-terminal amino
acid sequence.";
RL FEBS Lett. 144:349-353(1982).
RN [8]
RP SEQUENCE OF 20-198.
RX MEDLINE=81184038; PubMed=6164372;
RA Takagi T., Takagi K., Kawai T.;
RT "Complete amino acid sequence of human alpha 1-microglobulin.";
RL Biochem. Biophys. Res. Commun. 98:997-1001(1981).
RN [9]
RP SEQUENCE OF 206-350.
RX MEDLINE=85225968; PubMed=2408638;
RA Reisinger P., Hochstrasser K., Albrecht G.J., Lempart K.,
Salier J.-P.;
RT "Human inter-alpha-trypsin inhibitor: localization of the kunitz-type
domains in the N-terminal part of the molecule and their release by a
trypsin-like proteinase.";
RL Biol. Chem. Hoppe-Seyler 366:479-483(1985).
RN [10]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=82074265; PubMed=6171497;
RA Hochstrasser K., Schoenberger O.L., Rosemanith I., Wachter E.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
the inter-alpha-trypsin inhibitor. V. Attachments of carbohydrates in
the human urinary trypsin inhibitor isolated by affinity
chromatography.";
RL Hoppe-Seyler's Z. Physiol. Chem. 362:1357-1362(1981).
RN [11]
RP INHIBITORY SITE.
RX MEDLINE=85225940; PubMed=3890890;
RA Morli M., Travis J.;
RT "The reactive site of human inter-alpha-trypsin inhibitor is in the
amino-terminal half of the protein.";
RL Biol. Chem. Hoppe-Seyler 366:19-21(1985).
RN [12]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=90306345; PubMed=1694784; DOI=10.1016/0014-5793(90)81531-R;
RA Escibano J., Lopez-Otin C., Hjerpe A., Grubb A.O., Mendez E.;
RT "Location and characterization of the three carbohydrate prosthetic
groups of human protein HC.";
RL FEBS Lett. 266:167-170(1990).
RN [13]
RP BINDING TO CHROMOPHORE.
RX MEDLINE=91340714; PubMed=1714898;
RA Escibano J., Grubb A.O., Calero M., Mendez E.;
RT "The protein HC chromophore is linked to the cysteine residue at
position 34 of the polypeptide chain by a reduction-resistant bond and
causes the charge heterogeneity of protein HC.";
RL J. Biol. Chem. 266:15758-15763(1991).
RN [14]
RP BINDING TO CHROMOPHORE.
RX MEDLINE=20095837; PubMed=10631976;
RA Berggard T., Cohen A., Persson P., Lindqvist A., Cedervall T.,
Silow M., Thøgersen I.B., Jonsson J.A., Enghild J.J., Akström B.;
RT "Alpha1-microglobulin chromophores are located to three lysine
residues embedded in the lipocalin pocket and associated with a
novel lipophilic compound.";
RL Protein Sci. 8:2611-2620(1999).
RN [15]
RP SEQUENCE OF 206-219, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.
RC TISSUE=Plasma;
RX MEDLINE=94229087; PubMed=7513643;
RA Morelle W., Capon C., Baldyck M., Sautiere P., Kouach M.,
Michalek C., Fournet B., Mizon J.;
RT "Chondroitin sulphate covalently cross-links the three polypeptide
chains of inter-alpha-trypsin inhibitor.";
RL Eur. J. Biochem. 221:881-888(1994).
RN [16]
RP SEQUENCE OF 206-223, AND CROSS-LINK SITE TO HC2.
RX MEDLINE=9332026; PubMed=768253;
RA Enghild J.J., Salvesen G., Thøgersen I.B., Valnickova Z., Pizzo S.V.,
Hefza S.A.;
RT "Presence of the protein-glycosaminoglycan-protein covalent cross-link
in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain
2/bikunin.";

RL J. Biol. Chem. 268:8711-8716(1993).
RN [17]
RP SEQUENCE OF 206-223, AND CROSS-LINK SITE TO HC3.
RX MEDLINE=91093267; PubMed=1898736;
RA Enghild J.J., Salvesen G., Helto S.A., Thøgersen I.B., Rutherford S.,
RA Pizzo S.V.;
RT "Chondroitin 4-sulfate covalently cross-links the chains of the human
RT blood protein pre-alpha-inhibitor.";
RL J. Biol. Chem. 266:747-751(1991).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 230-339.
RX MEDLINE=96227321; PubMed=9566199; DOI=10.1006/jmbi.1997.1582;
RA Xu Y., Carr P.D., Guss J.M., Ollis D.L.;
RT "The crystal structure of bikunin from the inter-alpha-inhibitor
RT complex: a serine protease inhibitor with two Kunitz domains.";
RL J. Mol. Biol. 276:955-966(1998).
RN [19]
RP REVIEW.
RX MEDLINE=20513981; PubMed=11058759;
RA Akersroem B., Loegberg L., Berggard T., Osmark P., Lindqvist A.;
RT "Alpha(1)-microglobulin: a yellow-brown lipocalin.";
RL Biochim. Biophys. Acta 1482:172-184(2000).
CC -I- FUNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with IGA
CC and albumin.
CC -I- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase.
CC -I- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-alpha-1) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-alpha-LI) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-alpha-1) of H3 and bikunin (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -I- PTM: The precursor is proteolytically processed into two
CC separately functioning proteins.
CC -I- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
CC chromophores.
CC -I- PTM: Addition of glycosaminoglycan chondroitin sulfate, allows
CC cross-linking between the different components.
CC -I- MISCELLANEOUS: In vitro, the first twelve residues of the amino
CC
Query Match 90.0%; Score 296; DB 1; Length 352;
Best Local Similarity 92.7%; Pred. No. 6,5e-27;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ACNLPVAGPCIAFPFNAFDVAKGCVLPYGGCGGNGNKRYSKECEYGVGP 56
DB 286 ACNLPVAGPCIAFPFNAFDVAKGCVLPYGGCGGNGNKRYSKECEYGVGP 340
RESULT 3
AMBP PIG
ID AMBP PIG STANDARD; PRT; 337 AA.
AC P04366; P34954;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
DE trypsin inhibitor light chain (ITI-LC) (bikunin) (H1-30) (E1-14)]
DE (Fragment).
GN Name=AMBP; Synonyms=ITIL;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBT_Taxid=9823;
RX SEQUENCE FROM N.A.
RX MEDLINE=90353595; PubMed=1696914; DOI=10.1016/0014-5793(90)81112-2;
RX Gebhard W., Schreitmüller T., Vetr H., Wachter E., Hochstrasser K.;

RT RT
RT "Complementary DNA and deduced amino acid sequences of porcine alpha
RT 1-microglobulin and bikunin.";
RL FEBS Lett. 269:32-36(1990).
RN [2]
RP SEQUENCE OF 2-337 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91113729; PubMed=1703444; DOI=10.1016/0167-4781(91)90152-C;
RA Tavakoli A.;
RT "Molecular cloning of porcine alpha 1-microglobulin/H1-30 reveals
RT developmental and tissue-specific expression of two variant messenger
RT ribonucleic acids.";
RL Biochim. Biophys. Acta 1088:47-56(1991).
RN [3]
RP SEQUENCE OF 212-334.
RX MEDLINE=8525967; PubMed=2408637;
RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RT inhibitors.";
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC -I- FUNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with IGA
CC and albumin.
CC -I- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase.
CC -I- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-alpha-1) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-alpha-LI) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-alpha-1) of H3 and bikunin (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -I- PTM: The precursor is proteolytically processed into two
CC separately functioning proteins.
CC -I- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
CC chromophores (By similarity).
CC -I- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -I- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
DR EMBL; X53685; CAA37725.1; -;
DR EMBL; X52087; CAA36306.1; -;
DR PIR; S11066; TTPGBI.
DR HGSP; P02760; TBP1.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019855; F:calcium channel inhibitor activity; ISS.
DR GO; GO:0046904; F:calcium oxalate binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0019862; F:IGA binding; ISS.
DR GO; GO:0030568; F:plasmin inhibitor activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0030304; F:trypsin inhibitor activity; ISS.
DR GO; GO:0030236; P:anti-inflammatory response; ISS.
DR GO; GO:0007155; P:cell adhesion; ISS.
DR GO; GO:0042167; P:heme catabolism; ISS.
DR GO; GO:0050777; P:negative regulation of immune response; ISS.
DR GO; GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO; GO:0007565; P:pregnancy; ISS.
DR InterPro; IPR002968; A1-microglobulin.
DR InterPro; IPR011038; Calycin.

DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR000566; Lipocln cytfABP.
 DR InterPro: IPR002223; Prot inh_Kunz-m.
 DR Pfam: PF00014; Kunitz_BPTI; 2.
 DR Pfam: PF00061; Lipocalin_1.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRINTS: PR00179; LIPOCALIN.
 DR ProDom: PD000222; Prot_Inh_Kunz-m; 2.
 DR SMART: SM00131; KU; 2.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
 DR PROSITE: PS00213; LIPOCALIN; 1.
 DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
 KW Serine protease inhibitor; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 4 By similarity.
 FT CHAIN 5 188 Alpha-1-microglobulin.
 FT CHAIN 191 337 Inter-alpha-trypsin inhibitor light chain.
 FT DOMAIN 216 266 BPTI/Kunitz inhibitor 1.
 FT BINDING 272 332 BPTI/Kunitz inhibitor 2.
 FT BINDING 38 38 Chromophore (By similarity).
 FT BINDING 96 96 Chromophore (By similarity).
 FT BINDING 122 132 Chromophore (By similarity).
 FT BINDING 134 144 Chromophore (By similarity).
 FT BINDING 176 173 Chromophore (By similarity).
 FT DISULFID 216 266 By similarity.
 FT DISULFID 225 249
 FT DISULFID 241 262
 FT DISULFID 272 332
 FT DISULFID 281 305
 FT DISULFID 297 318
 FT CARBOHYD 100 100
 FT CARBOHYD 235 235
 FT SITE 226 227 N-linked (GlcNAc...) (potential).
 FT SITE 282 283 Inhibitory (P1) (chymotrypsin, elastase).
 FT SITE 282 283 Inhibitory (P1) (trypsin).
 FT CONFLICT 49 49 T -> M (in Ref. 2).
 FT CONFLICT 259 259 E -> Q (in Ref. 3).
 FT CONFLICT 270 270 E -> S (in Ref. 3).
 FT CONFLICT 278 278 S -> Q (in Ref. 3).
 FT CONFLICT 283 283 G -> A (in Ref. 3).
 FT CONFLICT 286 286 FQ -> IR (in Ref. 3).
 FT CONFLICT 293 293 V -> A (in Ref. 3).
 FT CONFLICT 311 311 Q -> K (in Ref. 3).
 FT CONFLICT 315 315 E -> Q (in Ref. 3).
 SQ SEQUENCE 337 AA; 37690 MW; 1F630FF98E3CD10F CRC64;

Query Match 82.7%; Score 272; DB 1; Length 337;
 Best Local Similarity 82.1%; Pred. No. 4.4e-24;
 Matches 46; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCLAFPPRAFDVAKGKCTLPFGGCGGNGNKFYSKEGRCYGV 56
 DB 270 EACSLPIVSGPCRGFPQWAFVAGKCVLFNNGCGGNGNPFYSKEGRCYGV 325

RESULT 4
 AMBP_BOVIN STANDARD; PRT; 352 AA.
 ID AMBP_BOVIN P00978; P35420; Q28020;
 AC P00978; P35420; Q28020;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE AMBP protein precursor [contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (H1-30) (BI-14) (Cumulus extracellular matrix stabilizing factor) (ESF)].
 GN Name=AMBP; Synonyms=ITIL;
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Lindqvist A., Akerstrom B.,
 RT "Bovine alpha 1-microglobulin/bikunin. Isolation and characterization of liver cDNA and urinary alpha 1-microglobulin.",
 RL Biochim. Biophys. Acta 1306:98-106(1996).
 RN [12]
 RP SEQUENCE OF 227-349.
 RX MEDLINE=85225967; PubMed=2408637;
 RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor. X. The amino-acid sequences of the trypsin-released inhibitors from horse and pig inter-alpha-trypsin inhibitors.",
 RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
 RN [13]
 RP SEQUENCE OF 227-348.
 RX MEDLINE=84133807; PubMed=6199275;
 RA Hochstrasser K., Wachter E.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor. VII. Determination of the amino-acid sequence of the trypsin-released inhibitor from bovine inter-alpha-trypsin inhibitor.",
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983).
 RN [4]
 RP SEQUENCE OF 206-219.
 RC TISSUE=Fetal serum;
 RX MEDLINE=92291130; PubMed=1376324;
 RA Chen L., Mao S.J.T., Larsen W.J.;
 RT "Identification of a factor in fetal bovine serum that stabilizes the cumulus extracellular matrix. A role for a member of the inter-alpha-trypsin inhibitor family.",
 RL J. Biol. Chem. 267:12380-12386(1992).
 RN [5]
 RP REACTIVE SITES.
 RX MEDLINE=84133808; PubMed=6199276;
 RA Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor. VII. Characterization of the bovine inhibitor as double-headed trypsin-elastase inhibitor.",
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:1689-1696(1983).
 CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological fluids including plasma, urine, and cerebrospinal fluid. It appears not only as a free monomer but also in complexes with IgA and albumin.
 CC -1- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and urine, inhibits trypsin, plasmin, and lysosomal granulocytic elastase.
 CC -1- FUNCTION: May diffuse into follicular fluid after an ovulatory stimulus to act as structural linker that ensure normal cumulus expansion, through stabilization of the cumulus extracellular matrix thus supporting the process of ovulation.
 CC -1- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-alpha-1) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-alpha-1i) of H2 and bikunin, and pre-alpha-inhibitor (P-alpha-1) of H3 and bikunin (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- PTM: The precursor is proteolytically processed into two separately functioning proteins.
 CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow chromophores (By similarity).
 CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin family.
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL, U35642; AAB07599.1; -
 DR PIR, S68149; TIBOBI.
 DR HSSP, P02760; IBIK.
 DR GO, GO:0005576; C:extracellular; ISS.
 DR GO, GO:0005886; C:plasma membrane; ISS.
 DR GO, GO:0019855; F:calcium channel inhibitor activity; ISS.
 DR GO, GO:0046904; F:calcium oxalate binding; ISS.
 DR GO, GO:0020037; F:heme binding; ISS.
 DR GO, GO:0019862; F:IgA binding; ISS.
 DR GO, GO:0030568; F:plasmin inhibitor activity; ISS.
 DR GO, GO:0042803; F:protein homodimerization activity; ISS.
 DR GO, GO:0030304; F:trypsin inhibitor activity; ISS.
 DR GO, GO:0030236; F:anti-inflammatory response; ISS.
 DR GO, GO:0007155; P:cell adhesion; ISS.
 DR GO, GO:0042167; P:heme catabolism; ISS.
 DR GO, GO:0050777; P:negative regulation of immune response; ISS.
 DR GO, GO:0046329; P:negative regulation of JNK cascade; ISS.
 DR GO, GO:0007565; P:pregnancy; ISS.
 DR InterPro, IPR002968; A1-microglobulin.
 DR InterPro, IPR011038; Calycin.
 DR InterPro, IPR002345; Lipocalin.
 DR InterPro, IPR00566; Lipocalin cytochrome.
 DR InterPro, IPR002223; Prot. Inh_Kunz-m.
 DR Pfam, PF00014; Kunitz_BPTI; 2.
 DR Pfam, PF00061; Lipocalin; 1.
 DR PRINTS, PR00759; BASICPTASE.
 DR PRINTS, PR00179; LIPOCALIN.
 DR ProDom, PD000222; Prot. Inh_Kunz-m; 2.
 DR SMART, SM00131; KU; 2.
 DR PROSITE, PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE, PS0279; BPTI_KUNITZ_2; 2.
 DR PROSITE, PS00213; LIPOCALIN; 1.
 DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
 KW Serine protease inhibitor; Signal.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 203 Alpha-1-microglobulin.
 FT CHAIN 206 352 Inter-alpha-trypsin inhibitor light chain.
 FT DOMAIN 231 281 BPTI/Kunitz inhibitor 1.
 FT BINDING 287 337 BPTI/Kunitz inhibitor 2.
 FT BINDING 53 53 Chromophore (By similarity).
 FT BINDING 111 111 Chromophore (By similarity).
 FT BINDING 137 137 Chromophore (By similarity).
 FT BINDING 149 149 Chromophore (By similarity).
 FT DISULFID 91 188 By similarity.
 FT DISULFID 231 281 By similarity.
 FT DISULFID 240 264 By similarity.
 FT DISULFID 256 277 By similarity.
 FT DISULFID 287 337 By similarity.
 FT DISULFID 296 320 By similarity.
 FT DISULFID 312 333 By similarity.
 FT SITE 241 242 Inhibitory (PI) (chymotrypsin, elastase).
 FT SITE 297 298 Inhibitory (PI) (trypsin).
 FT CARBOHYD 115 115 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 223 223 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 250 250 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 209 209 T->G (in Ref. 4).
 FT CONFLICT 217 217 A->D (in Ref. 4).
 FT CONFLICT 268 268 G->L (in Ref. 2 and 3).
 FT CONFLICT 274 274 E->Q (in Ref. 2 and 3).
 FT CONFLICT 298 299 SY->AP (in Ref. 2 and 3).
 FT CONFLICT 330 330 SY->Q (in Ref. 2 and 3).
 FT CONFLICT 346 346 E->R (in Ref. 2 and 3).
 FT SEQUENCE 352 AA; 39235 MW; EDJ1C5CA02E70B19 CRC64;

Query Match 81.8%; Score 269; DB 1; Length 352;
 Best Local Similarity 78.6%; Pred. No. 1e-23; Mismatches 6; Indels 0; Gaps 0;

Oy 1 EACNLPVGRPCIAFPFPMADAVKGCULFPYGGCGQNGNKFYSKECREYCGVP 56
 Db 285 EACNLPVGRPCRSYIQMAFDAYKGVKCRYSYGCKGNKFTYSKECKEYCGIP 340

RESULT 5
 IATR_HORSE STANDARD; PRT; 125 AA.
 AC P04355.
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Inter-alpha-trypsin inhibitor (Irt) (HI-14) (Inhibitory
 DE fragment of Irt) (Fragment).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE OF 3-125.
 RX MEDLINE=85225967; PubMed=2408637;
 RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
 RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
 RT the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
 RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
 RT inhibitors";
 RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
 RN [2]
 RP SEQUENCE OF 1-31.
 RC TISSUE=urine;
 RX PubMed=1627153;
 RA Veeragavan K., Singh K., Wachter E., Hochstrasser K.;
 RT "Characterization of a trypsin inhibitor from equine urine";
 RL Biochem. Int. 26:405-413(1992).
 CC -1- FUNCTION: This inhibitory fragment, released from native Irt after
 CC limited proteolysis with trypsin, contains two homologous domains.
 CC Whereas the second domain is a strong inhibitor of trypsin, the
 CC first domain interacts weakly with PMN-granulocytic elastase and
 CC not at all with pancreatic elastase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: The amino acid at position p2' (17) appears to
 CC determine the specificity of the inhibition of domain I.
 CC Inhibitors with methionine in this position interact weakly with
 CC chymotrypsin and elastase; those with leucine interact strongly.
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR PIR, A01210; TIBOBI.
 DR HSSP, P02760; IBIK.
 DR InterPro, IPR002223; Prot. Inh_Kunz-m.
 DR Pfam, PF00014; Kunitz_BPTI; 2.
 DR PRINTS, PR00759; BASICPTASE.
 DR ProDom, PD000222; Prot. Inh_Kunz-m; 2.
 DR SMART, SM00131; KU; 2.
 DR PROSITE, PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE, PS0279; BPTI_KUNITZ_2; 2.
 KW Direct protein sequencing; Glycoprotein; Plasma; Repeat;
 KW Serine protease inhibitor.
 FT NON TER 1 1
 FT DOMAIN 7 57 BPTI/Kunitz inhibitor 1.
 FT DOMAIN 63 113 BPTI/Kunitz inhibitor 2.
 FT SITE 17 18 Reactive bond for chymotrypsin and
 FT SITE 17 18 elastase.
 FT SITE 73 74 Reactive bond for trypsin.
 FT DISULFID 7 57
 FT DISULFID 16 40
 FT DISULFID 32 53
 FT DISULFID 63 113
 FT DISULFID 72 96
 FT DISULFID 88 109
 FT CARBOHYD 26 26
 FT CONFLICT 13 13 N-linked (GlcNAc...)
 FT CONFLICT 125 125 Q->E (in Ref. 2).
 FT NON TER 125 125
 FT SEQUENCE 125 AA; 13725 MW; CE79B4D801DF42D5 CRC64;


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RESULT 7
ID 0925W1 PRELIMINARY; PRT; 349 AA.
AC 0925W1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Alpha-1-microglobulin/bikunin precursor (BMEh1.2.1) (Alpha 1
microglobulin/bikunin, variant 1).
GN Name=Ambp; Synonyms=AMBP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99326507; PubMed=10395906; DOI=10.1016/S0378-1119(99)00191-2;
RA Lindqvist A., Rouet P., Salier J.P., Akerstrom B.;
RT "The alpha-1-microglobulin/bikunin gene: characterization in mouse and
evolution.";
RL Gene 234:329-336(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Rahs S.S., Loggiani N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boake S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
Villalón D.K., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the lipocalin family.
DR EMBL, AF034692; AAD01995.1; -
DR EMBL, BC021660; AAH21660.1; -
DR EMBL, AL691496; CAD83043.1; -
DR HSSP, P02760, 1BIK.
DR MGD, MGI:88002; Ambp.
DR GO, GO:0005615; C:extracellular space; TAS.
DR GO, GO:0005886; C:plasma membrane; ISS.
DR GO, GO:0019855; F:calcium channel inhibitor activity; ISS.
DR GO, GO:0046904; F:calcium channel binding; ISS.
DR GO, GO:0020037; F:heme binding; ISS.
DR GO, GO:0019862; F:IGA binding; ISS.
DR GO, GO:0030568; F:plasmin inhibitor activity; ISS.
DR GO, GO:0048003; F:protein homodimerization activity; ISS.
DR GO, GO:0030304; F:trypsin inhibitor activity; ISS.

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DR GO, GO:0030236; P:anti-inflammatory response; ISS.
DR GO, GO:0007155; P:cell adhesion; ISS.
DR GO, GO:0042167; P:heme catabolism; ISS.
DR GO, GO:0050777; P:negative regulation of immune response; ISS.
DR GO, GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO, GO:0007565; P:pregnancy; ISS.
DR Pfam, PF00014; Kunitz_BPT1; 2.
DR Pfam, PF00061; Lipocalin; 1.
DR PRINTS, PR01215; ALMOGLOBULIN.
DR PRINTS, PR00759; BASICPRASE.
DR PRINTS, PR00179; LIPOCALIN.
DR PRODOM, PD000222; Prot_Inh_Kunz-m; 2.
DR SMART, SM00131; KU; 2.
DR PROSITE, PS00280; BPT1_KUNITZ_1; 2.
DR PROSITE, PS00279; BPT1_KUNITZ_2; 2.
DR PROSITE, PS00213; LIPOCALIN; UNKNOWN_1.
DR LIPOCALIN; Signal.
DR SIGNAL 1 19 Potential.
FT CHAIN 20 349 alpha-1-microglobulin/bikunin.
SQ SEQUENCE 349 AA; 39029 MW; CFE9208D37DF0021 CRC64;

Query Match 79.3%; Score 261; DB 2; Length 349;
Best Local Similarity 78.2%; Pred. No. 9.2e-23;
Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 2 ACNLPYVGPCLAFPPRWAFPAVKGCYLPFYGGCGGNGNRPYSEKREYCGVP 56
DB 265 ACNLPYVGPCLAFPPRWAFPAVKGCYLPFYGGCGGNGNRPYSEKREYCGVP 339

RESULT 8
ID 09DBJ9 PRELIMINARY; PRT; 349 AA.
AC 09DBJ9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus adult male liver cDNA, RIKEN full-length enriched
library, clone:1300004018 product:alpha 1 microglobulin/bikunin, full
insert sequence.
DE insert sequence.
GN Name=Ambp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RT Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:11757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RA Akechi T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imocani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurahara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
 RA Sogae Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka M.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the lipocalin family.
 CC -1- SIMILARITY: Contains 2 BPT/Kunitz inhibitor domains.
 DR EMBL: AK004907; BMB23659.1; -.
 DR HSSP: P02760; IBIK.
 DR MGD: MGI:88002; Ambp.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0005865; C:plasma membrane; ISS.
 DR GO: GO:0019855; F:calcium channel inhibitor activity; ISS.
 DR GO: GO:0046904; F:calcium oxalate binding; ISS.
 DR GO: GO:0020037; P:heme binding; ISS.
 DR GO: GO:0019862; P:IGA binding; ISS.
 DR GO: GO:0030568; P:plasmin inhibitor activity; ISS.
 DR GO: GO:0042803; F:protein homodimerization activity; ISS.
 DR GO: GO:0030304; F:trypsin inhibitor activity; ISS.
 DR GO: GO:0030236; P:anti-inflammatory response; ISS.
 DR GO: GO:0007155; P:cell adhesion; ISS.
 DR GO: GO:0042167; P:heme catabolism; ISS.
 DR GO: GO:0050777; P:negative regulation of immune response; ISS.
 DR GO: GO:0046329; P:negative regulation of JNK cascade; ISS.
 DR GO: GO:0007565; P:pregnancy; ISS.
 DR InterPro: IPR002968; AI-microglobln.
 DR InterPro: IPR011038; Calycin.
 DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR000566; Lipocalin cyFABP.
 DR InterPro: IPR002223; ProtInh_Kunz-m.
 DR Pfam: PF00014; Kunitz_BPT1; 2.
 DR Pfam: PF00061; Lipocalin_1.
 DR PRINTS: PR01215; A1MCGLOBULIN.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD000222; ProtInh_Kunz-m; 2.
 DR SMART: SM00131; KU; 2.
 DR PROSITE: PS00280; BPT1_KUNITZ_1; 2.
 DR PROSITE: PS00279; BPT1_KUNITZ_2; 2.
 DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
 KW Lipocalin.
 SQ SEQUENCE 349 AA; 39101 MW; E592222FBC01BCGD CRG64;

Query Match 79.3%; Score 261; DB 2; Length 349;
 Best Local Similarity 78.2%; Pred. No. 9; 2e-23;
 Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACNLPVAGPCIAEPFPAWVAGKCYLPFYGGCGGNGNKFYSKEKREYCGVP 56
 DB 285 ACNLPVAGPCIAEPFPAWVAGKCYLPFYGGCGGNGNKFYSKEKREYCGVP 339
 RESULT 9
 AMBP_MERUN STANDARD; PRT; 346 AA.
 ID AMBP_MERUN 062577; 062576;
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
 DE trypsin inhibitor light chain (Irr-LC) (Bikunin) (HI-30)].
 CN Name=ABMP; Synonyms=ITIL;
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC Meriones.
 OX NCBI_TaxID=10047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95110820; PubMed=7529051; DOI=10.1016/0167-4838(94)90198-8;
 RA Ide H., Itoh H., Nawa Y.,
 RT "Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
 RT Mongolian gerbil and Syrian golden hamster in comparison with man and
 RT other species."
 RL Biochim. Biophys. Acta 1209:286-292(1994).
 CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
 CC fluids including plasma, urine, and cerebrospinal fluid. It
 CC appears not only as a free monomer but also in complexes with IGA
 CC and albumin (By similarity).
 CC -1- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
 CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
 CC elastase (By similarity).
 CC -1- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
 CC one or two heavy chains (H1, H2 or H3) and one light chain,
 CC bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
 CC and bikunin, inter-alpha-like inhibitor (I-alpha-II) of H2 and
 CC bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- PTM: The precursor is proteolytically processed into two
 CC separately functioning proteins.
 CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
 CC chromophores (By similarity).
 CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
 CC family.
 CC -1- SIMILARITY: Contains 2 BPT/Kunitz inhibitor domains.
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: D31813; BAA0600.1; -.
 DR HSSP: P02760; IBIK.
 DR GO: GO:0005576; C:extracellular space; ISS.
 DR GO: GO:0005865; C:plasma membrane; ISS.
 DR GO: GO:0019855; F:calcium channel inhibitor activity; ISS.
 DR GO: GO:0046904; F:calcium oxalate binding; ISS.
 DR GO: GO:0020037; P:heme binding; ISS.
 DR GO: GO:0019862; P:IGA binding; ISS.
 DR GO: GO:0030568; P:plasmin inhibitor activity; ISS.
 DR GO: GO:0042803; F:protein homodimerization activity; ISS.
 DR GO: GO:0030304; F:trypsin inhibitor activity; ISS.
 DR GO: GO:0030236; P:anti-inflammatory response; ISS.

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DR GO:0007155; P:cell adhesion; ISS.
DR GO:0042167; P:heme catabolism; ISS.
DR GO:0050777; P:negative regulation of immune response; ISS.
DR GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO:0007565; P:pregnancy; ISS.
DR InterPro: IPR002968; A1-microglobulin.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR000566; Lipocalin cytochrome P450.
DR InterPro: IPR002223; Protein Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 2.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00179; LIPOCALIN.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
KW Glycoprotein; Lipocalin; Plasma; Repeat; Serine protease inhibitor;
KW Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 202 Inter-alpha-tryptsin inhibitor light
FT CHAIN 205 346 chain.
FT DOMAIN 230 280 BPTI/Kunitz inhibitor 1.
FT DOMAIN 286 336 BPTI/Kunitz inhibitor 2.
FT BINDING 52 52 Chromophore (By similarity).
FT BINDING 110 110 Chromophore (By similarity).
FT BINDING 136 136 Chromophore (By similarity).
FT BINDING 148 148 Chromophore (By similarity).
FT DISULFID 90 187 By similarity.
FT DISULFID 230 280 By similarity.
FT DISULFID 239 263 By similarity.
FT DISULFID 255 276 By similarity.
FT DISULFID 286 336 By similarity.
FT DISULFID 295 319 By similarity.
FT DISULFID 311 332 By similarity.
FT CARBOHYD 114 114 N-linked (GlcNAc...) (potential).
FT CARBOHYD 249 249 N-linked (GlcNAc...) (potential).
FT SITE 240 241 Inhibitory (PI) (chymotrypsin, elastase)
FT SITE 296 297 (By similarity).
FT SITE 297 Inhibitory (PI) (trypsin) (By
FT SITE 297 similarity).
SQ SEQUENCE 346 AA; 38643 MW; F1A463810918D5F CRC64;
Query Match 78.7%; Score 259; DB 1; Length 346;
Best Local Similarity 76.4%; Pred. No. 1.6e-22;
Matches 42; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
OY 2 ACNLEPIVGPCTAFPPRNFAVDKVKCVLPYGGCGGNGNKKFSREKREYCGVP 56
DB 285 ACNLEPIVGPCTAFPPRNFAVDKVKCVLPYGGCGGNGNKKFSREKREYCGVP 339

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RT "Rat alpha 1-microglobulin: co-expression in liver with the light
RT chain of inter-alpha-tryptsin inhibitor.";
RT Biochim. Biophys. Acta 1130:63-67(1992).
RN [2]
RP SEQUENCE OF 141-195 FROM N.A.
RX MEDLINE=87033744; PubMed=2429663;
RA Kastern W., Bjorck L., Aakerstrom B.;
RT "Developmental and tissue-specific expression of alpha 1-microglobulin
RT mRNA in the rat.";
RL J. Biol. Chem. 261:15070-15074(1986).
RN [3]
RP SEQUENCE OF 283-343, AND CHARACTERIZATION.
RC STRAIN=Miscar;
RX MEDLINE=89053978; PubMed=3263966;
RA Kido H., Yokogoshi Y., Katunuma N.;
RT "Kunitz-type protease inhibitor found in rat mast cells. Purification,
RT properties, and amino acid sequence.";
RL J. Biol. Chem. 263:18104-18107(1988).
RN [4]
RP PROCESSING.
RX MEDLINE=9414892; PubMed=7508921;
RA Itoh H., Ide H., Ishikawa N., Nawa Y.;
RT "Mast cell protease inhibitor, tryptstatin, is a fragment of inter-
RT alpha-tryptsin inhibitor light chain.";
RL J. Biol. Chem. 269:3818-3822(1994).
CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with Iga
CC and albumin (By similarity).
CC -1- FUNCTION: Inter-alpha-tryptsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase (By similarity).
CC -1- FUNCTION: Tryptstatin is a trypsin inhibitor. It inhibits blood
CC coagulation factor Xa and trypsin about 100-fold more rapidly
CC than porcine pancreatic trypsin and chymase. It is a monomer but
CC is also found in mast cells as a complex with trypsin.
CC -1- SUBUNIT: I-alpha-I plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-alpha-I) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Synthesized in the liver and secreted in
CC plasma. Tryptstatin is present in mast cell granules.
CC -1- PTM: The precursor is proteolytically processed into two
CC separately functioning proteins.
CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
CC chromophores (By similarity).
CC -1- PTM: Heavy chains are interlinked with bikunin via a chondroitin
CC 4-sulfate bridge to the their C-terminal aspartate (By
CC similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S87544; AAB21782.1; -.
DR EMBL: J02600; AAA41596.1; -.
DR PIR: S21089; S21089.
DR HSSP: P02760; 1BTK.
DR RGD: 2102; Ambp.
DR GO:0005576; C:extracellular; ISS.
DR GO:0005886; C:plasma membrane; ISS.
DR GO:0019855; F:calcium channel inhibitor activity; ISS.
DR GO:0046904; F:calcium oxalate binding; ISS.

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DR GO; GO:0020037; F-heme binding; ISS.
 DR GO; GO:0019862; F-iga binding; ISS.
 DR GO; GO:0030562; F-plasmin inhibitor activity; ISS.
 DR GO; GO:0042803; F-protein homodimerization activity; ISS.
 DR GO; GO:0030304; F-trypsin inhibitor activity; ISS.
 DR GO; GO:0030236; Plant-inflamatory response; ISS.
 DR GO; GO:0007155; P-cell adhesion; ISS.
 DR GO; GO:0042167; P-heme catabolism; ISS.
 DR GO; GO:0050777; P-negative regulation of immune response; ISS.
 DR GO; GO:0046329; P-negative regulation of JNK cascade; ISS.
 DR GO; GO:0007565; P-pregnancy; ISS.
 DR InterPro; IPR002968; A1-microglobulin.
 DR InterPro; IPR011038; Calycin.
 DR InterPro; IPR002345; Lipocalin.
 DR InterPro; IPR000566; Lipocalin cytochrome P-450.
 DR InterPro; IPR002223; Prot Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 2.
 DR Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PR00179; BASICPTASE.
 DR PRINTS; PR00179; LIPOCALIN.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
 KW Serine protease inhibitor; Signal.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 202 Alpha-1-microglobulin.
 FT CHAIN 205 349 Inter-alpha-trypsin inhibitor light chain.
 FT CHAIN 263 343 Trypsatin.
 FT DOMAIN 230 280 BPTI/Kunitz inhibitor 1.
 FT BINDING 286 336 BPTI/Kunitz inhibitor 2.
 FT BINDING 52 52 Chromophore (By similarity).
 FT BINDING 110 110 Chromophore (By similarity).
 FT BINDING 136 136 Chromophore (By similarity).
 FT BINDING 148 148 Chromophore (By similarity).
 FT DISULFID 90 187 By similarity.
 FT DISULFID 230 280 By similarity.
 FT DISULFID 239 263 By similarity.
 FT DISULFID 255 276 By similarity.
 FT DISULFID 286 336 By similarity.
 FT DISULFID 295 319 By similarity.
 FT DISULFID 311 332 By similarity.
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 233 233 N-linked (GlcNAc...) (potential).
 FT SITE 240 241 Inhibitory (PI) (chymotrypsin, elastase) (By similarity).
 FT SITE 296 297 Inhibitory (PI) (trypsin) (By similarity).
 FT CONFLICT 142 142 G -> A (in Ref. 2).
 FT CONFLICT 302 302 W -> L (in Ref. 3).
 FT CONFLICT 323 323 G -> N (in Ref. 3).
 FT CONFLICT 330 331 KE -> PK (in Ref. 3).
 FT CONFLICT 334 334 E -> W (in Ref. 3).
 SQ SEQUENCE 349 AA; 38851 MW; 187FB7DCB0824E01 CRC64;

Query Match 78.4%; Score 258; DB 1; Length 349;
 Best Local Similarity 78.2%; Pred. No. 2.1e-22;
 Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

DB 2 ACNLPVIRGPCIAFFPRMADFVAVKGVLPFYGGCGGNGKFKFSEKREYCGVP 56
 285 ACNLPVIRGPCIAFFPRMADFVAVKGVLPFYGGCGGNGKFKFSEKREYCGVP 339

RESULT 11
 IATR_CAPHI STANDARD; PRT; 123 AA.
 AC P62756; P13371;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Inter-alpha-trypsin inhibitor (ITI) (GIR-14) (Inhibitory fragment of ITI) (Fragment)
 DE ITI (Fragment)
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae; Caprinae; Capra.
 OC Caprinae; Capra.
 OC NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9105540; PubMed=2481505; DOI=10.1016/0167-4838(89)90017-4;
 RA Raap G., Hochstrasser K., Gerl C., Wachter E.;
 RT "Primary structure of a proteinase inhibitor released from goat serum inter-alpha-trypsin inhibitor."
 RT Biochim. Biophys. Acta 999:335-337(1989).
 CC -I- FUNCTION: This inhibitory fragment, released from native ITI after limited proteolysis with trypsin, contains two homologous domains. Whereas the second domain is a strong inhibitor of trypsin, the first domain interacts weakly with PMN-granulocytic elastase and not at all with pancreatic elastase.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- MISCELLANEOUS: The amino acid at position p2' (17) appears to determine the specificity of the inhibition of domain I inhibitors with methionine in this position interact weakly with chymotrypsin and elastase; those with leucine interact strongly.
 CC -I- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR HSSP; P02760; 1BIK.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 2.
 DR PRINTS; PR00179; BASICPTASE.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
 DR Direct protein sequencing; Glycoprotein; Plasma; Repeat;
 KW Serine protease inhibitor.
 FT NON_TER 1 1
 FT DOMAIN 5 55 BPTI/Kunitz inhibitor 1.
 FT DOMAIN 61 111 BPTI/Kunitz inhibitor 2.
 FT SITE 15 16 Reactive bond for chymotrypsin and elastase.
 FT SITE 71 72 Reactive bond for trypsin.
 FT DISULFID 5 55 By similarity.
 FT DISULFID 14 38 By similarity.
 FT DISULFID 30 51 By similarity.
 FT DISULFID 61 111 By similarity.
 FT DISULFID 70 94 By similarity.
 FT DISULFID 86 107 By similarity.
 FT CARBOHYD 24 24 N-linked (GlcNAc...)
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13686 MW; 295038173F22D2D1 CRC64;

Query Match 78.1%; Score 257; DB 1; Length 123;
 Best Local Similarity 76.8%; Pred. No. 1.1e-22;
 Matches 43; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

DB 1 EACNLPVIRGPCIAFFPRMADFVAVKGVLPFYGGCGGNGKFKFSEKREYCGVP 56
 59 EACNLPVIRGPCIAFFPRMADFVAVKGVLPFYGGCGGNGKFKFSEKREYCGVP 114

RESULT 12
 IATR_SHEEP STANDARD; PRT; 123 AA.
 AC P62757; P13371;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Inter-alpha-trypsin inhibitor (ITI) (Inhibitory fragment of ITI) (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae; Caprinae; Ovis.
 OC Caprinae; Ovis.

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OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=87299012; PubMed=2441725;
RA Raap G., Hochstrasser K., Wächter E., Reisinger P.W.M.;
RT "The amino-acid sequence of the trypsin-released inhibitor from sheep
RT Inter-alpha-trypsin inhibitor.";
RL Biol. Chem. Hoppe-Seyler 368:727-731(1987).
CC -1- FUNCTION: This inhibitory fragment, released from native ITI after
CC limited proteolysis with trypsin, contains two homologous domains.
CC Whereas the second domain is a strong inhibitor of trypsin, the
CC first domain interacts weakly with PMN-granulocytic elastase and
CC not at all with pancreatic elastase.
CC -1- MISCELLANEOUS: The amino acid at position p2' (17) appears to
CC determine the specificity of the inhibition of domain I.
CC Inhibitors with methionine in this position interact weakly with
CC chymotrypsin and elastase; those with leucine interact strongly.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC PIR, A29652; A29652.
DR HSSP, P02760; IBIK.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI_2.
DR PRINTS, PR00759; BASICPTASE.
DR SMART, SMO0131; KU; 2.
DR PROSITE, PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE, PS00279; BPTI_KUNITZ_2; 2.
KW Direct protein sequencing; Glycoprotein; Plasma; Repeat;
KM Serine protease inhibitor.
FT NON_TER 1 1
FT DOMAIN 5 55 BPTI/Kunitz inhibitor 1.
FT DOMAIN 61 111 BPTI/Kunitz inhibitor 2.
FT SITE 15 16 Reactive bond for chymotrypsin and
FT SITE 71 72 Reactive bond for trypsin.
FT DISULFID 5 55 By similarity.
FT DISULFID 14 58 By similarity.
FT DISULFID 30 51 By similarity.
FT DISULFID 61 111 By similarity.
FT DISULFID 70 94 By similarity.
FT DISULFID 86 107 By similarity.
FT CAROHD 24 24 N-linked (GlcNAc... ).
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13686 MW; 295038173F2D2D1 CRC64;
Query Match 78.1%; Score 257; DB 1; Length 123;
Best Local Similarity 76.8%; Pred. No. 1,1e-22;
Matches 43; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
Cy 1 EACNLPYVRGPIAFPPWAPDAVKGKCVLPYGGCGGNGNKFYSKEGREGYGPV 56
Db 59 QACNLPYVRGPIAFPPWAPDAVKGKCVLPYGGCGGNGNKFYSKEGREGYGPV 114

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RT RT "Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
RT Mongolian gerbil and Syrian golden hamster in comparison with man and
RT other species.";
RL Biochim. Biophys. Acta 1209:286-292(1994).
RN [2]
RP SEQUENCE OF 205-348, AND SUBUNITS.
RX TISSUE=Plasma, and Urine;
RC MEDLINE=97018241; PubMed=8864857;
RA Yamamoto T., Yamamoto K., Sinozawa H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
RT hamster urine and plasma.";
RL J. Biochem. 120:145-152(1996).
CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with Iga
CC and albumin (By similarity).
CC -1- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase (By similarity).
CC -1- FUNCTION: Trypsin is a trypsin inhibitor. It inhibits blood
CC coagulation factor Xa and trypsin about 100-fold more rapidly
CC than porcine pancreatic trypsin and chymase. It is a monomer but
CC is also found in mast cells as a complex with tryptase (By
CC similarity).
CC -1- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-alpha-II) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- PTM: The precursor is proteolytically processed into separately
CC functioning proteins.
CC -1- PTM: Alpha-1-microglobulin contains a covalently linked brown-
CC yellow chromophore (By similarity).
CC -1- PTM: Heavy chains are interlinked with bikunin via a chondroitin
CC 4-sulfate bridge to the their C-terminal aspartate (By
CC similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC -----
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CC or send an email to license@sib.ch).
CC -----
DR EMBL, D31814; BA006601.1; -.
DR HSSP, P02760; IBIK.
DR GO: GO:0005576; C:extracellular; ISS.
DR GO: GO:0005886; C:plasma membrane; ISS.
DR GO: GO:0019855; F:calcium channel inhibitor activity; ISS.
DR GO: GO:0046904; F:calcium oxalate binding; ISS.
DR GO: GO:0020037; F:heme binding; ISS.
DR GO: GO:0019862; F:Iga binding; ISS.
DR GO: GO:0030568; F:plasmin inhibitor activity; ISS.
DR GO: GO:0042803; F:protein homodimerization activity; ISS.
DR GO: GO:0030304; F:trypsin inhibitor activity; ISS.
DR GO: GO:0030236; F:anti-inflammatory response; ISS.
DR GO: GO:0007155; P:cell adhesion; ISS.
DR GO: GO:0042167; P:heme catabolism; ISS.
DR GO: GO:0050777; P:negative regulation of immune response; ISS.
DR GO: GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO: GO:0007565; P:pregnancy; ISS.
DR InterPro: IPR002968; A1-microglobln.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR000566; Lipocalin_cytrFAP.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.

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DR Pfam; PF00014; Kunitz BPTI; 2.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR Direct protein sequencing; Glycoprotein; Lipocalin; Plasma; Repeat;
KM Serine protease inhibitor; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 202 Alpha-1-microglobulin.
FT CHAIN 205 349 Inter-alpha-trypsin inhibitor light
FT chain.
FT CHAIN 282 349 Trypsin.
FT DOMAIN 230 280 BPTI/Kunitz inhibitor 1.
FT DOMAIN 236 336 BPTI/Kunitz inhibitor 2.
FT BINDING 52 52 Chromophore (By similarity).
FT BINDING 110 110 Chromophore (By similarity).
FT BINDING 136 136 Chromophore (By similarity).
FT BINDING 148 148 Chromophore (By similarity).
FT DISULFID 90 187 By similarity.
FT DISULFID 230 280 By similarity.
FT DISULFID 239 263 By similarity.
FT DISULFID 255 276 By similarity.
FT DISULFID 266 336 By similarity.
FT DISULFID 295 319 By similarity.
FT DISULFID 311 332 By similarity.
FT CARBOHYD 35 35 N-linked (GlcNAc...) (potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (potential).
FT SITE 240 241 Inhibitory (P1) (chymotrypsin, elastase)
FT SITE 296 297 Inhibitory (P1) (trypsin) (By
FT similarity).
FT CONFLICT 342 342 G -> E (in Ref. 2).
SQ SEQUENCE 349 AA; 38782 MW; 8C954584B7DBE728 CRC64;

Query Match 77.2%; Score 254; DB 1; Length 349;
Best Local Similarity 76.4%; Pred. No. 6.2e-22;
Matches 42; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFFPRWAFDAVKGCVLPFYGGCGGNGNKFYSEKCEKCYGVP 56
DB 285 ACSLPVIRGPCRAVYELWAFDAQGCKVQPSYGGCGGNGNKFYSEKCEKCYGVP 339

RESULT 14
ID 070160 PRELIMINARY; PRT; 352 AA.
AC 070160;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 26, Last sequence update)
DE Alpha-1-microglobulin/bikunin.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBT_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Liver;
RA Yoshida K., Suzuki Y., Yamamoto K., Sinohara H.;
RT "Guinea pig alpha1-microglobulin/bikunin: cDNA sequencing, tissue
expression and expression during acute phase.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 122:165-172(1999).
CC 1-SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AB006444; BAA25305.1; -.
DR HSSP; P02760; 1BTK.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019855; F:calcium channel inhibitor activity; ISS.
DR GO; GO:0046904; F:calcium oxalate binding; ISS.

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DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0019862; F:IGA binding; ISS.
DR GO; GO:0030568; F:plasmin inhibitor activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0030304; F:trypsin inhibitor activity; ISS.
DR GO; GO:0030236; F:anti-inflammatory response; ISS.
DR GO; GO:0004267; P:heme catabolism; ISS.
DR GO; GO:0050777; P:negative regulation of immune response; ISS.
DR GO; GO:0046329; P:negative regulation of JNK cascade; ISS.
DR GO; GO:0007565; P:pregnancy; ISS.
DR InterPro; IPR002968; A1-microglobulin.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocalin cytochrome P.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR01215; ALMOGLOBULIN.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN.
SQ SEQUENCE 352 AA; 39033 MW; BAA7447B574C2FAB CRC64;

Query Match 76.9%; Score 253; DB 2; Length 352;
Best Local Similarity 78.2%; Pred. No. 8.3e-22;
Matches 43; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFFPRWAFDAVKGCVLPFYGGCGGNGNKFYSEKCEKCYGVP 56
DB 286 ACNLPVIRGPCGSAQLWAFDAIKGCVRFYGGCGGNGNKFYSEKCEKCYGVP 340

RESULT 15
ID 06P2V8 PRELIMINARY; PRT; 342 AA.
AC 06P2V8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein MG76314.
GN Name=MG76314;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBT_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerard D.S.;
 RL Submitted (Dec-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the lipocalin family.
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR EMBL: BC064278; AAH64278.1; -
 DR HSSP: P10646; IADZ.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR GO: GO:0005215; P:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR002968; A1-microglobulin.
 DR InterPro: IPR011038; Calycin.
 DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR005566; Lipocalin_cytfabp.
 DR InterPro: IPR002223; Prot_inh_Kunz-m.
 DR Pfam: PF00014; Kunitz_BPTI; 2.
 DR Pfam: PF00061; Lipocalin; 1.
 DR PRINTS: PR01215; A1MCGLOBULIN.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRINTS: PR00179; LIPOCALIN.
 DR ProDom: PD000222; Prot_inh_Kunz-m; 2.
 DR SMART: SM00131; KU; 2.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
 DR PROSITE: PS00213; LIPOCALIN; 1.
 DR Hypothetical protein; Lipocalin.
 SO SEQUENCE 342 AA; 38191 MW; D9B5B5B25C8CB5A CRC64;

Query Match 70.5%; Score 232; DB 2; Length 342;
 Best Local Similarity 72.2%; Pred. No. 2.5e-19;
 Matches 39; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRWAFDAVKGCYLFPYGGCGGNGNKFYSEKCEKREYCGV 55
 Db 280 ACRLEPTGPGCAKTHWAFDAQCKCVTFAYGGCGGNGNNGFYTEKCEKREYCGV 333

RESULT 16
 P70004 PRELIMINARY; PRT; 342 AA.
 AC P70004;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Alpha1-microglobulin/bikunin precursor (AMBP).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 RA Kawahara A., Hikosaka A., Sasado T., Hirota K.;
 RL "Thyroid hormone-dependent repression of alpha1-microglobulin/bikunin
 (AMBP) gene expression during amphibian metamorphosis.";
 RL Dev. Genes Evol. 206:355-362(1997).
 CC -1- SIMILARITY: Belongs to the lipocalin family.
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR EMBL: D87752; BA13453.1; -
 DR HSSP: P02760; IBTK.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR GO: GO:0005215; P:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR002968; A1-microglobulin.
 DR InterPro: IPR011038; Calycin.
 DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR005566; Lipocalin_cytfabp.
 DR InterPro: IPR002223; Prot_inh_Kunz-m.
 DR Pfam: PF00014; Kunitz_BPTI; 2.

DR Pfam: PF00061; Lipocalin; 1.
 DR PRINTS: PR01215; A1MCGLOBULIN.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRINTS: PR00179; LIPOCALIN.
 DR ProDom: PD000222; Prot_inh_Kunz-m; 2.
 DR SMART: SM00131; KU; 2.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 2.
 DR PROSITE: PS00213; LIPOCALIN; 1.
 DR Lipocalin; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 342 Potential.
 SO SEQUENCE 342 AA; 38558 MW; 3050508BDCSC47B CRC64;

Query Match 69.3%; Score 228; DB 2; Length 342;
 Best Local Similarity 70.4%; Pred. No. 7.5e-19;
 Matches 38; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRWAFDAVKGCYLFPYGGCGGNGNKFYSEKCEKREYCGV 55
 Db 280 ACRLEPTGPGCAKTHWAFDAQCKCVTFAYGGCGGNGNNGFYTEKCEKREYCGV 333

RESULT 17
 Q7S246 PRELIMINARY; PRT; 342 AA.
 ID Q7S246;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Ambp-prov protein.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscil T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.,
 RL "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RL "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Klein S., Strausberg R.,

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the lipocalin family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: BC054142; AAH54142.1; -.
DR HSSP: P02760; 1BIK.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transporter, IEA.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR000566; Lipocalin_cyFABP.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF00014; Kunitz BPTI; 2.
DR Pfam: PF00061; Lipocalin; 1.
DR ProDom: PD000222; Prot_inh_Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE: PS00213; LIPOCALIN; 1.
KW Lipocalin.
SQ SEQUENCE 342 AA; 38549 MW; BA18FA543B7D4481 CRC64;

Query Match 69.3%; Score 228; DB 2; Length 342;
Best Local Similarity 70.4%; Pred. No. 7.5e-19;
Matches 38; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 ACNLPVHGRCIAFPFPMFAVDKGCYLFPPYGGCGGNGNKFYSKREYCGV 55
DB 280 ACRLLPPTPCPKTAKTHWAFDAAGKCVTFSTGGCGGNGNPFYTKREYCGV 333

RESULT 18
ID P78492 PRELIMINARY; PRT; 51 AA.
AC P78492;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Inter-alpha-trypsin inhibitor (Fragment).
GN Name=ITIL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86025577; PubMed=2413856;
RA Bourguignon J., Diarra-Mehrpour M., Sesboue R., Fraiz M.,
RA Sala-Trepat J.M., Martin J.P., Saller J.P.;
RT "Human inter-alpha-trypsin-inhibitor: characterization and partial
nucleotide sequencing of a light chain encoding cDNA.",
RL Biochem Biophys Res Commun. 131:1146-1153(1985).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: M11562; AAA59194.1; -.
DR HSSP: P02760; 1BIK.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF00014; Kunitz BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
FT NON_TER 1 1
SQ SEQUENCE 51 AA; 5698 MW; C13D74054D45EED2 CRC64;

Query Match 69.0%; Score 227; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 WAFDAVKGKCVLFPPYGGCGGNGNKFYSKREYCGV 56
DB 2 WAFDAVKGKCVLFPPYGGCGGNGNKFYSKREYCGV 39

RESULT 19
ID Q7SXH6 PRELIMINARY; PRT; 216 AA.
AC Q7SXH6;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Similar to alpha-1-microglobulin/bikunin.
GN ORFNames=sgc.66321;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bock S.A., McKernan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schain J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: BC055598; AAH55598.1; -.
DR HSSP: P02760; 1BIK.
DR ZFIN: ZDB-GENE-040426-1608; zgc:66321.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transporter; IEA.
DR InterPro: IPR011038; Calycin.
DR InterPro: IPR002223; Prot_inh_Kunz-m.
DR Pfam: PF00014; Kunitz BPTI; 2.
DR ProDom: PD000222; Prot_inh_Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 2.
SQ SEQUENCE 216 AA; 23835 MW; 9E951B4BF0245706 CRC64;

Query Match 62.9%; Score 207; DB 2; Length 216;
Best Local Similarity 64.2%; Pred. No. 1.6e-16;
Matches 34; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 2 ACNLPVHGRCIAFPFPMFAVDKGCYLFPPYGGCGGNGNKFYSKREYCGV 54
DB 150 ACRLLPMDAGPKAFVDMWAFDSSGKCLSTKYGCGGNGNPFYSKREYCGV 202

RESULT 20
ID Q6ZNI4 PRELIMINARY; PRT; 283 AA.
Q6ZNI4


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DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULFIDE CORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match
Best Local Similarity 55.3%; Score 182; DB 2; Length 576;
Matches 29; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 ACNLPVRGPCIAPFPMAFDVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
DB 385 ACSLPALQPCAKAYPRMAYNSQTGCGSFVYGGCEGNGNPFESRACECSCPP 439

RESULT 23
ID Q7LDM0 PRELIMINARY; PRT; 571 AA.
AC Q7LDM0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth and differentiation factor-associated serum protein 1.
GN Name-Gaspl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C;
RA MEDLINE=22656519; PubMed=12595574; DOI=10.1210/me.2002-0366;
RA Hill J.C., Qiu Y., Hewick R.M., Wolfman N.M.;
RT "Regulation of myostatin in vivo by growth and differentiation factor-
RT associated serum protein-1: a novel protein with protease inhibitor
RT and follistatin domains.";
RL Mol. Endocrinol. 17:1144-1154(2003).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY308804; AAP72503.1; -.
DR HSSP; P00974; IK09.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0007179; P:transforming growth factor beta receptor si. .; IDA.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002223; Prot_Inh_Kazal.
DR InterPro; IPR011497; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.

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DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 571 AA; 63321 MW; B28E676B3DC71256 CRC64;

Query Match
Best Local Similarity 53.5%; Score 176; DB 2; Length 571;
Matches 28; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 3 CNLPVRGPCIAPFPMAFDVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
DB 381 CSLPALQPCAKAYPRMAYNSQTGCGSFVYGGCEGNGNPFESRACECSCPP 434

RESULT 24
ID Q7LDM0 PRELIMINARY; PRT; 491 AA.
AC Q7LDM0;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein RUD2 (Fragment).
GN Name=RUD2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21096910; PubMed=1157797; DOI=10.1093/hmg/10.4.339;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tutarelli C., Kearney L., Buckle V.T., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AB006464; AAK6123.1; -.
DR HSSP; Q16019; IAPV.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 491 AA; 52710 MW; 0E0954C8DB66206 CRC64;

Query Match
Best Local Similarity 52.3%; Score 172; DB 2; Length 491;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 BACNLPVRGPCIAPFPMAFDVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
DB 300 DACULPVGQPCAKAYPRMAYNSPLIQCHFPVYGGCEGNGNPFESRACECSCPP 355

RESULT 25

```

Q96NZ8
ID Q96NZ8 PRELIMINARY; PRT; 548 AA.
AC Q96NZ8; Q96NZ0;
DT 01-DEC-2001 (TRMBLrel. 19, Created)
DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DE Putative multivalent protease inhibitor WFIKN.
GN Name=WFIKN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyal L., Patchy L.;
RT "A human protein containing multiple types of protease-inhibitory
RT modulee."
RT Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
CC -i SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AF422194; AAL1883.1; -.
DR HSSP; P10646; IIRH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig-C2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; Igc2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
KW Protease.
SQ SEQUENCE 548 AA; 58798 MW; 72BB28708D3BFB1F CRC64;

Query Match 52.3%; Score 172; DB 2; Length 548;
Best Local Similarity 50.0%; Pred. No. 5.1e-12;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 EACNLPYVRGPIAPPRAPFAVAGKCVLPYGGCGGNGNKFYSRKEGREGVGP 56
DB 357 DACVLPAAVGGPCRGWPRWAPSPLLQQCHPFYVGGCGGNGNPFHSRSCEDACPVP 412

Search completed: February 23, 2005, 03:29:39
Job time : 80 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:35:06 ; Search time 2857 Seconds
(without alignments)
949.770 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPIYRGSCIAFFPRWA.....QGNGKFKYSEKREYCGVP 56

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Deiop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DEIOP=6 -DELEXT=7

Database : GenEmbl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	429	6	AX812179 Sequence
2	329	100.0	448	6	163562 Sequence 68
3	324	98.5	8584	6	163561 Sequence 66
4	324	98.5	8590	6	163563 Sequence 70

296	90.0	198	6	AR022173	AR022173 Sequence
296	90.0	198	6	111653	111653 Sequence 12
296	90.0	204	6	AR268979	AR268979 Sequence
296	90.0	209	6	AR022176	AR022176 Sequence
296	90.0	209	6	111656	111656 Sequence 15
296	90.0	210	6	AR022172	AR022172 Sequence
296	90.0	210	6	AR059722	AR059722 Sequence
296	90.0	210	6	111652	111652 Sequence 11
296	90.0	210	6	114720	114720 Sequence 74
296	90.0	210	6	113807	113807 Sequence 74
296	90.0	210	6	170519	170519 Sequence 74
296	90.0	295	6	AR022217	AR022217 Sequence
296	90.0	295	6	E04740	E04740 DNA encodin
296	90.0	295	6	111697	111697 Sequence 85
296	90.0	307	6	E05909	E05909 DNA encodin
296	90.0	313	6	AR022209	AR022209 Sequence
296	90.0	313	6	E04738	E04738 DNA encodin
296	90.0	313	6	111689	111689 Sequence 75
296	90.0	339	6	A31027	A31027 DNA for blk
296	90.0	339	6	A31028	A31028 DNA for blk
296	90.0	343	6	BD014127	BD014127 Proteinas
296	90.0	343	6	AR059724	AR059724 Sequence
296	90.0	343	6	E08412	E08412 DNA Sequence
296	90.0	344	6	114683	114683 Sequence 13
296	90.0	344	6	113770	113770 Sequence 13
296	90.0	344	6	170482	170482 Sequence 13
296	90.0	349	6	114678	114678 Sequence 13
296	90.0	349	6	112765	112765 Sequence 3
296	90.0	349	6	170477	170477 Sequence 3
296	90.0	350	6	AR022222	AR022222 Sequence
296	90.0	350	6	E04742	E04742 DNA encodin
296	90.0	350	6	111702	111702 Sequence 92
296	90.0	435	6	E13092	E13092 DNA encodin
296	90.0	441	6	AR268980	AR268980 Sequence
296	90.0	555	6	E12656	E12656 Synthetic D
296	90.0	624	6	AR275805	AR275805 Sequence
296	90.0	645	6	AR275818	AR275818 Sequence
296	90.0	666	6	AR275819	AR275819 Sequence
296	90.0	966	6	C0722922	C0722922 Sequence
296	90.0	1123	6	AX449677	AX449677 Sequence
296	90.0	1221	9	HSALM1CR	X04494 Human mRNA

ALIGNMENTS

RESULT 1
LOCUS AX812179 429 bp DNA linear PAT 02-DEC-2003
DEFINITION Sequence 3 from Patent WO03062431.
AX812179
VERSION AX812179.1 GI:38635810
KEYWORDS
SOURCE
ORGANISM
Pichia pastoris
Pichia pastoris
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE
AUTHORS Gerard,C., Poncin,A., Saubdray,F. and Petchot-Bacque,J.P.
TITLE Novel nucleotide sequences, gene constructs, expression vectors and
micro-organisms for secreting a protein such as epi-hne-4, and
epi-hne-4 protein obtained therefrom
JOURNAL Patent: WO 03062431-A 3 31-JUL-2003;
DEBIORHAW S.A. (CH)

FEATURES
source
Location/Qualifiers
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/organism="Pichia pastoris"
/mol_type="unassigned DNA"
/db_xref="taxon:4922"

CDS
1..426
/note="unamed protein product"
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/protein_id="CAE81809.1"
/db_xref="GI:38635811"

ORIGIN /translation="MRPSPITPAVLFAASALAAVNTTDETAQIPAAVIGSYDL
EGDFVAVLPEFNSITNGLLPINTTIAIAAEBSVLDKKACNLPIVRGPIAFPP
RMAFDVAVKCVLPFYGGGQGNKFTFSEKREKREVCVP"

Alignment Scores:
Pred. No.: 1.03e-32 Length: 429
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-038-722-27 (1-56) x AX812179 (1-429)

QY 1 GUAUAQYASAnleuProIleValArgGlyProCysIleAlaPhePheProArgTyrPala 20
Db 256 GAGGCTTGAACCTTGGCAATCGTCAGAGGTCCATGCAATGCTTTCTTCCCAAGATGGGCT 315
QY 21 PheAspAlaValIleGlyLysCysValIleuPheProTyrGlyCysGlnGlyAengly 40
Db 316 TTGCAAGCTGTAAAGGTAAAGTCCGCTTCTTCCCATCGGTGTTGTCAAGTAAAGGT 375
QY 41 AsnLysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 376 AACCAAGTCTACTCTGAGAGAGGTGTAAGAGTACTGTGTGTTCCA 423

RESULT 2

LOCUS 163562 448 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 68 from patent US 5663143.
ACCESSION 163562
VERSION 163562.1 GI:2481135
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 448)

AUTHORS Ley, A. Charles., Ladner, R. Charles., Guterman, S. Kosow.,
Roberts, B. Lindsay., Markland, W. and Kent, R. Baribault.
TITLE Engineered human-derived kunitz domains that inhibit human
neutrophil elastase

JOURNAL Patent: US 5663143-A 68 02-SEP-1997;
FEATURES Location/Qualifiers
1..448
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
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Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-038-722-27 (1-56) x I63562 (1-448)

QY 1 GUUAUAQYASAnleuProIleValArgGlyProCysIleAlaPhePheProArgTyrPala 20
Db 265 GAGGCTTGAACCTTGGCAATCGTCAGAGGTCCATGCAATGCTTTCTTCCCAAGATGGGCT 324
QY 21 PheAspAlaValIleGlyLysCysValIleuPheProTyrGlyCysGlnGlyAengly 40
Db 325 TTGCAAGCTGTAAAGGTAAAGTCCGCTTCTTCCCATCGGTGTTGTCAAGTAAAGGT 384
QY 41 AsnLysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 385 AACCAAGTCTACTCTGAGAGAGGTGTAAGAGTACTGTGTGTTCCA 432

RESULT 3

163561

LOCUS 163561 8584 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 66 from patent US 5663143.
ACCESSION 163561
VERSION 163561.1 GI:2481134
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 8584)
AUTHORS Ley, A. Charles., Ladner, R. Charles., Guterman, S. Kosow.,
Roberts, B. Lindsay., Markland, W. and Kent, R. Baribault.
TITLE Engineered human-derived kunitz domains that inhibit human
neutrophil elastase

JOURNAL Patent: US 5663143-A 66 02-SEP-1997;
FEATURES Location/Qualifiers
1..8584
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 7.18e-31 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: Gaps: 0

US-10-038-722-27 (1-56) x I63561 (1-8584)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTyrPalaPhe 21
Db 1212 GCTTGTACTTGGCAATCGTCAGAGGTCCATGCAATGCTTTCTTCCCAAGATGGGCTTTC 1271

QY 22 AspAlaValIleGlyLysCysValIleuPheProTyrGlyCysGlnGlyAenglyAsn 41
Db 1272 GACGCTGTAAAGGTAAAGTCCGCTTCTTCCCATACGCTGTGTGTCAAGTAAAGGTAAAC 1331

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 1332 AAGTCTTACTCTGAGAGAGGTGTAAGAGTACTGTGTGTTCCA 1376

RESULT 4

LOCUS 163563 8590 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 70 from patent US 5663143.
ACCESSION 163563
VERSION 163563.1 GI:2481136
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 8590)

AUTHORS Ley, A. Charles., Ladner, R. Charles., Guterman, S. Kosow.,
Roberts, B. Lindsay., Markland, W. and Kent, R. Baribault.
TITLE Engineered human-derived kunitz domains that inhibit human
neutrophil elastase

JOURNAL Patent: US 5663143-A 70 02-SEP-1997;
FEATURES Location/Qualifiers
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source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 7.18e-31 Length: 8590
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: Gaps: 0

US-10-038-722-27 (1-56) x I63563 (1-8590)

Oy	2	AlaCysAsnLeuProIleValArgIleProCysIleAlaPhePheProArgTrpAlaPhe	21
Db	1212	GCTTGAACCTTGCCCAATGATCGATGACAGAGTGCATGCTCTTCTTCCAGATGGACTTTC	1271
Oy	22	AspAlaValIlySGIlyLysCySvalIleuPheProTyrGIlyGIyCySGInGIyAsnGIyAsn	41
Db	1272	GACGCTGTTAAGGGTAAGTGGCTTGTGTTCCATAGCGGTGGTGTGCAGGTAAACGCTAAC	1331
Oy	42	LysPheTyrSerGIuLysGIuCySArgGIuTyrCySGIlyValPro	56
Db	1332	AAGTTCCTACTCGAGAGAGAGTGTAGAGATGCTGTGGTGTCCA	1376
RESULT 5			
LOCUS	AR022173	198 bp	linear
DEFINITION	Sequence 12 from patent US 5792629.		PAT 05-DEC-1998
ACCESSION	AR022173		
VERSION	AR022173.1		GI:3976235
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 198)		
TITLE	Morishita,H., Kanamori,T. and Nobuhara,M.		
JOURNAL	Isolated DNA encoding novel protease inhibitory polypeptide		
FEATURES	Patent: US 5792629-A 12 11-AUG-1998;		
source	location/Qualifiers		
	1..198		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
ALIGNMENT SCORES:			
Pred. No.:	8.37e-29	Length:	198
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
Db:	6	Gaps:	0
US-10-038-722-27 (1-56) x AR022173 (1-198)			
Oy	2	AlaCysAsnLeuProIleValArgIleProCysIleAlaPhePheProArgTrpAlaPhe	21
Db	10	GCTGTCATCTCCCATGATGTCGGGGCCCCCTGCCAGCCTTCATCCAGCTCTGGGCAATT	69
Oy	22	AspAlaValIlySGIlyLysCySvalIleuPheProTyrGIlyGIyCySGInGIyAsnGIyAsn	41
Db	70	GATGCTGTCAAGGGAGATGCGCTCTTCCCTTCAGGGGGCTGCCAGGGCAACCGGGAAC	129
Oy	42	LysPheTyrSerGIuLysGIuCySArgGIuTyrCySGIlyValPro	56
Db	130	AAGTTCCTACTCGAGAGAGAGTGCAGAGATGCTCGGGTGTCCCT	174
RESULT 6			
LOCUS	111653	198 bp	DNA
DEFINITION	Sequence 12 from Patent US 5409895.		linear
ACCESSION	111653		PAT 26-JUL-1995
VERSION	111653.1		GI:909171
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 198)		
TITLE	Morishita,H., Kanamori,T. and Nobuhara,M.		
JOURNAL	Protease inhibitory polypeptides derived from urinary trypsin		
FEATURES	inhibitor and compositions thereof		
source	Patent: US 5409895-A 12 25-APR-1995;		
	location/Qualifiers		
	1..198		
	/organism="unknown"		

ORIGIN	/mol_type="unassigned DNA"			
Alignment Scores:				
Pred. No.:	8.37e-29	Length:	198	
Score:	296.00	Matches:	51	
Percent Similarity:	92.73%	Conservative:	0	
Best Local Similarity:	92.73%	Mismatches:	4	
Query Match:	89.97%	Indels:	0	
DB:	6	Gaps:	0	
US-10-038-722-27 (1-56) x II1653 (1-198)				
OY	2	A1AcYsaenleupProlllevalArG1yProCysillealAphnePheProArGTrralAph	21	
DB	10	GCCGCAATCTCCCATATGTCGGGGCCCTCGCGAGCTTCATCCAGCTCTGGGCATTT	69	
OY	22	AspAlaVallylYsg1yLysCyValleuPheProTyrGlyGlyCySGInGlyAaNGlyAa	41	
DB	70	GATGCTGTCAAGGGGAAGTGTGCTCTCTTCCCTCAAGGGGCTGCAAGGCAAGGAAAC	129	
OY	42	LysPheTyrSerGlyLysGluCyArG1yTyrCySg1yValPro	56	
DB	130	AAGTTCTACTCAGAGAAGAGTGCAGAGTACGCGGTGTCCTT	174	
RESULT 7				
AR268979	LOCUS	AR268979	204 bp	DNA linear PAT 10-APR-2007
DEFINITION	Sequence 27 from patent US 6500646.			
ACCESSION	AR268979			
VERSION	AR268979.1 GI:29699795			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 204)			
AUTHORS	Kuriyama, S. and Hasegawa, T.			
TITLE	Cell membrane-directed drugs			
JOURNAL	Patent: US 6500646-A 27 31-DEC-2002;			
FEATURES	Location/Qualifiers			
source	1..204			
	/organism="unknown"			
	/mol_type="genomic DNA"			
ORIGIN				
Alignment Scores:				
Pred. No.:	8.61e-29	Length:	204	
Score:	296.00	Matches:	51	
Percent Similarity:	92.73%	Conservative:	0	
Best Local Similarity:	92.73%	Mismatches:	4	
Query Match:	89.97%	Indels:	0	
DB:	6	Gaps:	0	
US-10-038-722-27 (1-56) x AR268979 (1-204)				
OY	2	A1AcYsaenleupProlllevalArG1yProCysillealAphnePheProArGTrralAph	21	
DB	4	GCCGCAATCTCCCATATGTCGGGGCCCTCGCGAGCTTCATCCAGCTCTGGGCATTT	63	
OY	22	AspAlaVallylYsg1yLysCyValleuPheProTyrGlyGlyCySGInGlyAaNGlyAa	41	
DB	64	GATGCTGTCAAGGGGAAGTGTGCTCTCTTCCCTCAAGGGGCTGCAAGGCAAGGAAAC	123	
OY	42	LysPheTyrSerGlyLysGluCyArG1yTyrCySg1yValPro	56	
DB	124	AAGTTCTACTCAGAGAAGAGTGCAGAGTACGCGGTGTCCTT	168	
RESULT 8				
AR022176	LOCUS	AR022176	209 bp	DNA linear PAT 05-DEC-1998
DEFINITION	Sequence 15 from patent US 5792629.			
ACCESSION	AR022176			
VERSION	AR022176.1 GI:3976238			

KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 209)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.

TITLE Isolated DNA encoding novel protease inhibitory polypeptide

JOURNAL Patent: US 5792629-A 15 11-AUG-1998;

FEATURES

source 1. 209

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.8e-29 Length: 209
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x AR022176 (1-209)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21

DB 10 GCCTGCAATCTCCCATAGTCCGGGGCCCTGCCGAGCTTCATCAAGCTCTGGGCATT 69

QY 22 AppAlaValIleGlyIleCysValLeuPheProTyrGlyGlyCysGlnIleAsnGlyAsn 41

DB 70 GATGCTGTCAAGGGAGAGTGCCTCTCCCTACGGGGGGTGCACGGGCAACGGGAAC 129

QY 42 LysPheTyrSerGluIleGlyCysArgGlyTyrCysGlyValPro 56

DB 130 AAGTTCTACTCAGAGAGAGTGCAGAGTACTCGGCTGCTCCT 174

RESULT 9

LOCUS 111656 209 bp DNA linear PAT 26-JUL-1995

DEFINITION Sequence 15 from Patent US 5409895.

ACCESSION 111656

VERSION 111656.1 GI:909174

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 209)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.

TITLE Protease inhibitory polypeptides derived from urinary trypsin

JOURNAL Patent: US 5409895-A 15 25-APR-1995;

FEATURES

source 1. 209

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.8e-29 Length: 209
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x 111656 (1-209)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21

DB 10 GCCTGCAATCTCCCATAGTCCGGGGCCCTGCCGAGCTTCATCAAGCTCTGGGCATT 69

QY 22 AppAlaValIleGlyIleCysValLeuPheProTyrGlyGlyCysGlnIleAsnGlyAsn 41

DB 70 GATGCTGTCAAGGGAGAGTGCCTCTCCCTACGGGGGGTGCACGGGCAACGGGAAC 129

QY 42 LysPheTyrSerGluIleGlyCysArgGlyTyrCysGlyValPro 56

DB 130 AAGTTCTACTCAGAGAGAGTGCAGAGTACTCGGCTGCTCCT 174

RESULT 10

LOCUS AR022172 210 bp DNA linear PAT 05-DEC-1998

DEFINITION Sequence 11 from patent US 5792629.

ACCESSION AR022172

VERSION AR022172.1 GI:3976234

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 210)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.

TITLE Isolated DNA encoding novel protease inhibitory polypeptide

JOURNAL Patent: US 5792629-A 11 11-AUG-1998;

FEATURES

source 1. 210

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x AR022172 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21

DB 10 GCCTGCAATCTCCCATAGTCCGGGGCCCTGCCGAGCTTCATCAAGCTCTGGGCATT 69

QY 22 AppAlaValIleGlyIleCysValLeuPheProTyrGlyGlyCysGlnIleAsnGlyAsn 41

DB 70 GATGCTGTCAAGGGAGAGTGCCTCTCCCTACGGGGGGTGCACGGGCAACGGGAAC 129

QY 42 LysPheTyrSerGluIleGlyCysArgGlyTyrCysGlyValPro 56

DB 130 AAGTTCTACTCAGAGAGAGTGCAGAGTACTCGGCTGCTCCT 174

RESULT 11

LOCUS AR059722 210 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 24 from patent US 5840518.

ACCESSION AR059722

VERSION AR059722.1 GI:5986172

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 210)

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.

TITLE DNA fragment, vector containing the DNA fragment, transformant

transformed with the vector and process for producing protein using

JOURNAL Patent: US 5840518-A 24 24-NOV-1998;

FEATURES

source 1. 210

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51

Percent Similarity: 92.73%
Best Local Similarity: 92.73%
Query Match: 6 89.97%
Conservative: 0
Matches: 4
Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x AR059722 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCCGGGGCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIySGIyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGCAAGGGAGAGTGGCTCTTCCCTCAGGGGGCTGCCAGGGCAACGGGAAAC 129

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCCT 174

RESULT 12

LOCUS 111652 210 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 11 from Patent US 5409895.
ACCESSION 111652
VERSION 111652.1 GI:909170.
KEYWORDS
SOURCE Unknown.

REFERENCE 1 (bases 1 to 210)
AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
TITLE Protease inhibitory polypeptides derived from urinary trypsin inhibitor and compositions thereof
JOURNAL Patent: US 5409895-A 11 25-APR-1995;
FEATURES Location/Qualifiers
1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x 111652 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCCGGGGCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIySGIyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGCAAGGGAGAGTGGCTCTTCCCTCAGGGGGCTGCCAGGGCAACGGGAAAC 129

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCCT 174

RESULT 13

LOCUS 114720 210 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 74 from patent US 5451659.
ACCESSION 114720
VERSION 114720.1 GI:997203
KEYWORDS
SOURCE Unknown.

REFERENCE 1 (bases 1 to 210)
Unclassified.

AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
TITLE Polypeptide, DNA fragment encoding the same, drug composition containing the same and process for producing the same
JOURNAL Patent: US 5451659-A 74 19-SEP-1995;
FEATURES Location/Qualifiers
1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x 114720 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCCGGGGCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIySGIyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGCAAGGGAGAGTGGCTCTTCCCTCAGGGGGCTGCCAGGGCAACGGGAAAC 129

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCCT 174

RESULT 14

LOCUS 132807 210 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 74 from patent US 5589360.
ACCESSION 132807
VERSION 132807.1 GI:1823598
KEYWORDS
SOURCE Unknown.

REFERENCE 1 (bases 1 to 210)
AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
TITLE Polypeptide, DNA fragment encoding the same, drug composition containing the same and process for producing the same
JOURNAL Patent: US 5589360-A 74 31-DEC-1996;
FEATURES Location/Qualifiers
1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 8.84e-29 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x 132807 (1-210)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCCGGGGCCCTGCCAGGCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIySGIyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGCAAGGGAGAGTGGCTCTTCCCTCAGGGGGCTGCCAGGGCAACGGGAAAC 129

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCCT 174

Db 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTCTCCT 174

RESULT 15

LOCUS 170519

DEFINITION Sequence 74 from patent US 5679770.

ACCESSION 170519

VERSION 170519.1 GI:3006654

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 210)
Morishita, H., Kanamori, T. and Nobuhara, M.
Polypeptide, DNA fragment encoding the same, drug composition
containing the same and process for producing the same

JOURNAL Patent: US 5679770-A 74 21-OCT-1997;
Location/Qualifiers
1..210
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	8,84e-29	Length:	210
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x 170519 (1-210)

Qy 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21

Db 10 GCCTGCAATCTCCCATATGTCGGGGCCCCCTGCCAGCTTCATCCAGCTCTGGGCATT 69

Qy 22 AspaIaValIyGlyGlyCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

Db 70 GATGCTGTCAGAGGGAGAGTGCCTCTCCCTACGGGGGCTGCAGGGGCAACGGGAAC 129

Qy 42 LysPheTyrSerGlyGlyGlyCysArgGlyTyrCysGlyValPro 56

Db 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTCTCCT 174

RESULT 16

LOCUS AR022217

DEFINITION Sequence 85 from patent US 5792629.

ACCESSION AR022217

VERSION AR022217.1 GI:3976279

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 295)
Morishita, H., Kanamori, T. and Nobuhara, M.
Isolated DNA encoding novel protease inhibitory polypeptide
Patent: US 5792629-A 85 11-AUG-1998;
Location/Qualifiers
1..295
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	1.21e-28	Length:	295
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x AR022217 (1-295)

Qy 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21

Db 99 GCCTGCAATCTCCCATATGTCGGGGCCCCCTGCCAGCTTCATCCAGCTCTGGGCATT 158

Qy 22 AspaIaValIyGlyGlyCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

Db 159 GATGCTGTCAGAGGGAGAGTGCCTCTCCCTACGGGGGCTGCAGGGGCAACGGGAAC 218

Qy 42 LysPheTyrSerGlyGlyGlyCysArgGlyTyrCysGlyValPro 56

Db 219 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTCTCCT 263

RESULT 17

LOCUS E04740

DEFINITION DNA encoding novel protease inhibitor.

ACCESSION E04740

VERSION E04740.1 GI:2172936

KEYWORDS JP 1993084083-A/3.

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 295)
Morishita, H., Kanamori, T. and Nobuhara, M.
NEW POLYPEPTIDE, NEW DNA CODING THE SAME POLYPEPTIDE, PRODUCTION OF
NEW POLYPEPTIDE, NEW MEDICINE COMPOSITION AND NEW ENZYME INHIBITING
Patent: JP 1993084083-A 3 06-APR-1993;
WOCHIDA PHARMACEUT CO LTD

COMMENT

OS Artificial gene

OC Artificial sequence; Genes.

OS Escherichia coli

PN JP 1993084083-A/3

PD 06-APR-1993

PF 13-NOV-1991 JP 1991325220

PR 13-NOV-1990 JP 90P 306745

PI MORISHITA HIDEAKI, KANAMORI TOSHIYUKI, NOBUHARA MASAHIRO PC

CI2N15/15, A61K37/64, A61K37/64, A61K37/64, A61K37/64, A61K37/64, PC

A61K37/64

PC A61K37/64, A61K37/64, A61K37/64, C07K10, C12N1/21, C12N9/99, PC

CI2N15/70

PC C12P21/02, C12N1/21, C12R1.19, C12P21/02, C12R1.19, C07K99.00;

CC strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

CC *source: developmental_stage=rearranged;

*source: clone=PM551;

key Location/Qualifiers

FT 5'UTR 1..26

FT sig_peptide 27..89

FT mat_peptide 90..287

FT FT

291..295.

Location/Qualifiers

1..295

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

Alignment Scores:

Pred. No.:	1.21e-28	Length:	295
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x E04740 (1-295)

QY 2 AlaCysAsnLeuProIleValArgIleProCysIleAlaPheProArgTrrAlaPhe 21
 DB 99 GCGTGCATTCCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATTCACACTCGGGCATTT 158
 QY 22 AspaIaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 159 GATGCTGTCAAGGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCCAGGGGCAACCGGAAAC 218
 QY 42 LysPheTyrSerGluLysGluCysArgGluLysTyrCysGlyValPro 56
 DB 219 AAGTTTACTCAGAGAGAGTGCAGAGAGTACTGCGGTCTCCCT 263
 RESULT 18
 LOCUS 111697 295 bp DNA linear PAT 26-JUL-1995
 DEFINITION Sequence 85 from Patent US 5409895.
 ACCESSION 111697 GI:909215
 VERSION 111697.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 295)
 AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
 TITLE Protease inhibitory polypeptides derived from urinary trypsin inhibitor and compositions thereof
 JOURNAL Patent: US 5409895-A 85 25-Apr-1995;
 FEATURES
 source 1..295
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,21e-28 Length: 295
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 6 Gaps: 0
 US-10-038-722-27 (1-56) x 111697 (1-295)
 QY 2 AlaCysAsnLeuProIleValArgIleProCysIleAlaPheProArgTrrAlaPhe 21
 DB 99 GCGTGCATTCCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATTCACACTCGGGCATTT 158
 QY 22 AspaIaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 159 GATGCTGTCAAGGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCCAGGGGCAACCGGAAAC 218
 QY 42 LysPheTyrSerGluLysGluCysArgGluLysTyrCysGlyValPro 56
 DB 219 AAGTTTACTCAGAGAGAGTGCAGAGAGTACTGCGGTCTCCCT 263
 RESULT 19
 LOCUS E05909 307 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA encoding polypeptide which inhibits protease activity.
 ACCESSION E05909
 VERSION E05909.1 GI:2174096
 KEYWORDS JP 1993108988-A/1.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 307)
 AUTHORS Morishita,H., Kanamori,T. and Nobuhara,M.
 TITLE NEW POLYPEPTIDE, NEW DNA, NEW VECTOR, NEW TRANSFORMANT, NEW MEDICINAL COMPOSITION AND PRODUCTION OF THE NEW POLYPEPTIDE
 JOURNAL Patent: JP 1993108988-A 1 22-NOV-1993;
 MOCHIDA PHARMACEUT CO LTD
 COMMENT
 OS Artificial gene
 OC Artificial sequence; Genes.

OS Escherichia coli
 PN JP 1993108988-A/1
 PD 22-NOV-1993
 PF 12-MAY-1992 JP 1992146587
 PI MORISHITA HIDEAKI, KANAMORI TOSHIYUKI, NOBUHARA MASAHIRO PC
 C12P21/02,C12N15/00;
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key Location/Qualifiers
 FT 5'UTR 1..26
 FT 27..89
 FT Sig_peptide /product='signal peptide of
 FT /product='alkaliphosphatase'
 FT mac_peptide 90..293
 FT /product='polypeptide which inhibits protease
 FT activity,
 FT AN68',
 FT CDS 27..296
 FT /product='polypeptide which inhibits protease
 FT activity,
 FT AN68',
 FT 3'UTR 297..307
 FT replace(159..161,'')
 FT mutation /product='polypeptide which inhibits protease
 FT activity,
 FT v26del',
 FT mutation replace(246..248,'')
 FT /product='polypeptide which inhibits protease
 FT activity,
 FT v54del',
 FT FT
 FEATURES
 source 1..307
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,26e-28 Length: 307
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 6 Gaps: 0
 US-10-038-722-27 (1-56) x E05909 (1-307)
 QY 2 AlaCysAsnLeuProIleValArgIleProCysIleAlaPheProArgTrrAlaPhe 21
 DB 93 GCGTGTATCTACCAATAGTCCGGGGCCCTCCGAGCCTTCATTCACACTCGGGCATTT 152
 QY 22 AspaIaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 153 GATGCTGTCAAGGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCCAGGGGCAACCGGAAAC 212
 QY 42 LysPheTyrSerGluLysGluCysArgGluLysTyrCysGlyValPro 56
 DB 213 AAGTTTACTCAGAGAGAGTGCAGAGAGTACTGCGGTCTCCCT 257
 RESULT 20
 LOCUS AR022209 313 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 75 from patent US 5792629.
 ACCESSION AR022209
 VERSION AR022209.1 GI:3976271
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 313)

AUTHORS Morishita, H., Kanamori, T. and Nobuhara, M.
 TITLE Isolated DNA encoding novel protease inhibitory polypeptide
 JOURNAL Patent: US 5792629-A 75 11-AUG-1998;
 FEATURES Location/Qualifiers
 source 1..313
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-28	Length:	313
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x AR022209 (1-313)

QY 2 AlaCyAsnLeuProIleValArgIyProCySileAlaPhePheProArgTTPAlaPhe 21
 DB 99 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATT 158
 QY 22 AspaIaValIySGIyLVySCyValIeuPheProTyrgIyGlyCySGInGIyAsnGIyAsn 41
 DB 159 GATGCTGTCAGAGGGAAGTGCCTCTCTCCCTACGGGGGCTGCAGGGGAACGGGAAC 218
 QY 42 LysPheTySerGIuLySGIuCyArGIuTyrcySGIyValPro 56
 DB 219 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTCCCT 263

RESULT 21
 E04738 313 bp DNA linear PAT 29-SEP-1997
 LOCUS E04738
 DEFINITION DNA encoding novel protease inhibitor.
 ACCESSION E04738.1 GI:2172934
 VERSION JP 1993084083-A/1.
 KEYWORDS JP 1993084083-A/1.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 1 (bases 1 to 313)
 Morishita, H., Kanamori, T. and Nobuhara, M.
 AUTHORS NEW POLYPEPTIDE, NEW DNA CODING THE SAME POLYPEPTIDE, PRODUCTION OF
 TITLE NEW POLYPEPTIDE, NEW MEDICINE COMPOSITION AND NEW ENZYME INHIBITING
 JOURNAL Parent: JP 1993084083-A 1 06-APR-1993;
 MOCHIDA PHARMACEUT CO LTD
 COMMENT
 OS Artificial gene
 OS Artificial sequence; Genes.
 OS Escherichia coli
 PN JP 1993084083-A/1
 PD 06-APR-1993
 PF 13-NOV-1991 JP 1991325220
 PR 13-NOV-1990 JP 90P 306745
 PI MORISHITA HIDEAKI, KANAMORI TOSHIYUKI, NOBUHARA MASAHIRO PC
 C12N15/15, A61K37/64, A61K37/64, A61K37/64, A61K37/64, PC
 A61K37/64,
 PC A61K37/64, A61K37/64, A61K37/64, C07K7/10, C12N1/21, C12N9/99, PC
 C12N15/70,
 PC C12P21/02, (C12N1/21, C12R1:19), (C12P21/02, C12R1:19), C07K99:00;
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: developmental_stage=rearranged;
 CC *source: clone=PM552;
 FH Key Location/Qualifiers
 FT 5'UTR 1..26
 FT sig_peptide 27..89
 FT mat_peptide 90..299
 FT /product='novel protease inhibitor' FT 3'UTR
 FT 303..313.

FEATURES

Location/Qualifiers
 source 1..313
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-28	Length:	313
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x E04738 (1-313)

QY 2 AlaCyAsnLeuProIleValArgIyProCySileAlaPhePheProArgTTPAlaPhe 21
 DB 99 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATT 158
 QY 22 AspaIaValIySGIyLVySCyValIeuPheProTyrgIyGlyCySGInGIyAsnGIyAsn 41
 DB 159 GATGCTGTCAGAGGGAAGTGCCTCTCTCCCTACGGGGGCTGCAGGGGAACGGGAAC 218
 QY 42 LysPheTySerGIuLySGIuCyArGIuTyrcySGIyValPro 56
 DB 219 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTCCCT 263

RESULT 22
 I11689 313 bp DNA linear PAT 26-JUL-1995
 LOCUS I11689
 DEFINITION Sequence 75 from Patent US 5409895.
 ACCESSION I11689
 VERSION I11689.1 GI:909207
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 1 (bases 1 to 313)
 Morishita, H., Kanamori, T. and Nobuhara, M.
 AUTHORS Protease inhibitory polypeptides derived from urinary trypsin
 TITLE inhibitor and compositions thereof
 JOURNAL Patent: US 5409895-A 75 25-APR-1995;
 FEATURES Location/Qualifiers
 source 1..313
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-28	Length:	313
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	6	Gaps:	0

US-10-038-722-27 (1-56) x I11689 (1-313)

QY 2 AlaCyAsnLeuProIleValArgIyProCySileAlaPhePheProArgTTPAlaPhe 21
 DB 99 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATT 158
 QY 22 AspaIaValIySGIyLVySCyValIeuPheProTyrgIyGlyCySGInGIyAsnGIyAsn 41
 DB 159 GATGCTGTCAGAGGGAAGTGCCTCTCTCCCTACGGGGGCTGCAGGGGAACGGGAAC 218
 QY 42 LysPheTySerGIuLySGIuCyArGIuTyrcySGIyValPro 56
 DB 219 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTCCCT 263
 RESULT 23

AJ1027
LOCUS AJ1027 339 bp DNA linear PAT 21-AUG-1995
DEFINITION DNA for bikunin variant (domain II) from patent EP0401508.
ACCESSION AJ1027
VERSION AJ1027.1 GI:1249281
KEYWORDS
SOURCE
ORGANISM
other sequences: artificial sequences.
REFERENCE
1 (bases 1 to 339)
Fritz,H., Gebhard,W. and Das,R.
Proteinaseinhibitors, method for their preparation and
pharmaceutical compositions containing them
Patent: EP 0401508-A 12-DEC-1990;
JOURNAL
BAYER AG
FEATURES
source 1..339
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1,386-28 Length: 339
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
DB:
US-10-038-722-27 (1-56) x AJ1027 (1-339)
QY 2 AAlaCysaenleuprollevalaIArgGlyProCysilealaPhepheProArgTrrAlaPhe 21
Db 10 GCTGCAATCTCCCATAGTCCGAGGCCCTTCATCCAGCTCTGGGCATTT 69
QY 22 AepAlaValIySGIyLysCysValleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 70 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGGGGGCTGCCAAGGCAACGGGAAAC 129
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 174
RESULT 24
AJ1028/c 339 bp DNA linear PAT 21-AUG-1995
LOCUS AJ1028
DEFINITION DNA for bikunin variant (domain II) from patent EP0401508.
ACCESSION AJ1028
VERSION AJ1028.1 GI:1247246
KEYWORDS
SOURCE
ORGANISM
other sequences: artificial sequences.
REFERENCE
1 (bases 1 to 339)
Fritz,H., Gebhard,W. and Das,R.
Proteinaseinhibitors, method for their preparation and
pharmaceutical compositions containing them
Patent: EP 0401508-A 13-DEC-1990;
JOURNAL
BAYER AG
FEATURES
source 1..339
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1,386-28 Length: 339
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0

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QY 22 AepAlaValIySGIyLysCysValleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 270 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGGGGGCTGCCAAGGCAACGGGAAAC 211
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 210 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 166
RESULT 25
BD014127 339 bp DNA linear PAT 27-AUG-2002
LOCUS BD014127
DEFINITION Proteinase inhibitor, process for producing the same, and drug
containing it.
ACCESSION BD014127
VERSION BD014127.1 GI:22554456
KEYWORDS JP 2001112492-A/6.
SOURCE
ORGANISM
other sequences: artificial sequences.
REFERENCE
1 (bases 1 to 339)
Fritz,H., Gebhard,W. and Das,R.
Proteinase inhibitor, process for producing the same, and drug
containing it
Patent: JP 2001112492-A 6 24-APR-2001;
JOURNAL
BAYER AG
COMMENT
OS Artificial Sequence
PN JP 2001112492-A/6
PD 24-APR-2001
PF 13-SEP-2000 JP 2000278172
PR 13-MAY-1989 DE P3915689.3 18-JAN-1990 DE P4001244.1 PI
HANS FLITZ, WOLFGANG GERHARDT, RATHINORA DAS
PC C12N15/09,A61K38/55,A61P1/16,A61P7/00,A61P11/00, PC
A61P13/12,
PC A61P29/00,A61P43/00,C07K14/81,C12N9/99,C12P21/02,C12N15/00, PC
A61K37/64
CC variant of a second domain of bikunin
FH Key
FT source 1..339
Location/Qualifiers
FEATURES
source 1..339
/organism="Artificial Sequence"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1,386-28 Length: 339
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
DB:
US-10-038-722-27 (1-56) x BD014127 (1-339)
QY 2 AAlaCysaenleuprollevalaIArgGlyProCysilealaPhepheProArgTrrAlaPhe 21
Db 10 GCTGCAATCTCCCATAGTCCGAGGCCCTTCATCCAGCTCTGGGCATTT 69
QY 22 AepAlaValIySGIyLysCysValleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 70 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGGGGGCTGCCAAGGCAACGGGAAAC 129
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

Db 130 AGTCTACTCAGAGAGGAGTGCAGAGACTGGGGTCCCT 174

Search completed: February 23, 2005, 05:23:49
Job time : 2867 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 03:14:24 ; Search time 24 Seconds
(without alignments)
174.181 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPIVRGSCIAFFPRWA.....QGNGKFKYSEKREYCGVP 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	329	100.0	56	US-08-358-160-20	Sequence 20, Appl
2	329	100.0	141	US-08-358-160-69	Sequence 69, Appl
3	324	98.5	56	US-08-358-160-19	Sequence 19, Appl
4	324	98.5	141	US-08-358-160-69	Sequence 69, Appl
5	296	90.0	57	US-09-144-428-26	Sequence 26, Appl
6	296	90.0	58	US-07-700-526-14	Sequence 14, Appl
7	296	90.0	58	US-08-358-160-3	Sequence 3, Appl
8	296	90.0	58	US-08-358-160-75	Sequence 75, Appl
9	296	90.0	58	US-08-463-155A-39	Sequence 39, Appl
10	296	90.0	58	US-08-463-432B-39	Sequence 39, Appl
11	296	90.0	58	US-08-676-125A-47	Sequence 47, Appl
12	296	90.0	58	US-08-206-310A-39	Sequence 39, Appl
13	296	90.0	58	US-08-398-010A-39	Sequence 39, Appl
14	296	90.0	58	US-08-398-628A-39	Sequence 39, Appl
15	296	90.0	58	US-08-399-115A-39	Sequence 39, Appl
16	296	90.0	58	US-09-136-012A-47	Sequence 47, Appl
17	296	90.0	58	US-08-676-124-78	Sequence 78, Appl
18	296	90.0	58	US-09-414-878-78	Sequence 78, Appl
19	296	90.0	58	US-09-240-136-78	Sequence 78, Appl
20	296	90.0	58	US-09-638-770A-78	Sequence 78, Appl
21	296	90.0	58	PCR-US92-03132-11	Sequence 11, Appl
22	296	90.0	66	US-07-791-213D-8	Sequence 8, Appl
23	296	90.0	66	US-08-293-150A-8	Sequence 8, Appl
24	296	90.0	68	US-07-972-387-76	Sequence 76, Appl
25	296	90.0	68	US-08-431-412-76	Sequence 76, Appl
26	296	90.0	68	US-08-057-971-76	Sequence 76, Appl
27	296	90.0	68	US-08-235-515A-21	Sequence 21, Appl

28	296	90.0	68	US-09-331-793-23	Sequence 23, Appl
29	296	90.0	70	US-07-791-213D-3	Sequence 3, Appl
30	296	90.0	70	US-07-791-213D-6	Sequence 6, Appl
31	296	90.0	70	US-07-972-387-75	Sequence 75, Appl
32	296	90.0	70	US-08-431-412-75	Sequence 75, Appl
33	296	90.0	70	US-08-057-971-75	Sequence 75, Appl
34	296	90.0	70	US-08-293-150A-3	Sequence 3, Appl
35	296	90.0	70	US-08-293-150A-6	Sequence 6, Appl
36	296	90.0	70	US-08-235-515A-25	Sequence 25, Appl
37	296	90.0	87	US-07-791-213D-86	Sequence 86, Appl
38	296	90.0	87	US-08-293-150A-86	Sequence 86, Appl
39	296	90.0	89	US-07-972-387-14	Sequence 14, Appl
40	296	90.0	89	US-08-431-412-14	Sequence 14, Appl
41	296	90.0	89	US-08-057-971-14	Sequence 14, Appl
42	296	90.0	91	US-07-791-213D-76	Sequence 76, Appl
43	296	90.0	91	US-07-791-213D-93	Sequence 93, Appl
44	296	90.0	91	US-07-972-387-4	Sequence 4, Appl
45	296	90.0	91	US-08-431-412-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-358-160-20
Sequence 20, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KONITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iyer P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-20

Query Match 100.0%; Score 329; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.7e-26;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYRGPCIAFPFPMATDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56
DB 1 EACNLPYRGPCIAFPFPMATDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56

RESULT 2
US-08-358-160-69
Sequence 69, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

TELEX: 248633
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-69

Query Match 100.0%; Score 329; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYRGPCIAFPFPMATDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56
DB 86 EACNLPYRGPCIAFPFPMATDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 141

RESULT 3
US-08-358-160-19
Sequence 19, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-19

Query Match 98.5%; Score 324; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 ACNPIYVGPCTIAFPFPPWAFDAVVGKCYLFPYGGCGGNGNKFYSKECREYCGVP 56

RESULT 4
US-08-358-160-67

Sequence 67, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

TELEX: 248633
INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-67

Query Match 98.5%; Score 324; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.1e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNPIYVGPCTIAFPFPPWAFDAVVGKCYLFPYGGCGGNGNKFYSKECREYCGVP 56
Db 87 ACNPIYVGPCTIAFPFPPWAFDAVVGKCYLFPYGGCGGNGNKFYSKECREYCGVP 141

RESULT 5
US-09-144-428-26

Sequence 26, Application US/09144428
Patent No. 6583108

GENERAL INFORMATION:
APPLICANT: BAYER CORPORATION, The
APPLICANT: TAMBURINI, Paul P.
APPLICANT: DAVIS, Gary
APPLICANT: DELARIA, Katherine A.
APPLICANT: MARLOR, Christopher W.
APPLICANT: MULLER, Daniel K.
TITLE OF INVENTION: HUMAN BIKUNIN
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive Suite 3200
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,428
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/03894
FILING DATE: 10-MAR-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,106
FILING DATE: 11-MAR-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,793
FILING DATE: 14-JUN-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/725,251
FILING DATE: 04-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: CHAO, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 96,223-11

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 913-0001
TELEFAX: (312) 913-0002

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-144-428-26

Query Match 90.0%; Score 296; DB 4; Length 57;
Best Local Similarity 92.7%; Pred. No. 8, 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACNLPVIRGPCIAFPFPAFAVKGKCVLPFYGGCGGNGNKFSEKREYCGVP 56
DB 3 ACNLPVIRGPCRAFIQLWAFDAVKGKCVLPFYGGCGGNGNKFSEKREYCGVP 57

RESULT 6
US-07-700-526-11
; Sequence 11, Application US/07700526
; Patent No. 5166133
; GENERAL INFORMATION:
; APPLICANT: Houston, L. L.
; APPLICANT: Kaymakcalan, Zehra
; TITLE OF INVENTION: Method for Inhibiting Adhesion of White
; TITLE OF INVENTION: Blood Cells to Endothelial Cells
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/700,526
; FILING DATE: 19910816

ATTORNEY/AGENT INFORMATION:
; CLASSIFICATION: 424
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 2600.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3217
; TELEFAX: (415) 658-5239
; TELEX: 4992659
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-700-526-11

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACNLPVIRGPCIAFPFPAFAVKGKCVLPFYGGCGGNGNKFSEKREYCGVP 56
DB 2 ACNLPVIRGPCRAFIQLWAFDAVKGKCVLPFYGGCGGNGNKFSEKREYCGVP 56

RESULT 7
US-08-358-160-3
; Sequence 3, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-3

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACNLPVIRGPCIAFPFPAFAVKGKCVLPFYGGCGGNGNKFSEKREYCGVP 56
DB 4 ACNLPVIRGPCRAFIQLWAFDAVKGKCVLPFYGGCGGNGNKFSEKREYCGVP 58

RESULT 8
US-08-358-160-75
; Sequence 75, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEX=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-75

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23; 4; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPICIAFPFRRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEGREGYGV 56
DB 4 ACNLPYVGPICIAFPFRRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEGREGYGV 58

RESULT 9
US-08-463-155A-39
Sequence 39, Application US/08463155A
Patent No. 5780265
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,155A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-155A-39

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23; 4; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPICIAFPFRRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEGREGYGV 56
DB 4 ACNLPYVGPICIAFPFRRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEGREGYGV 58

RESULT 10
US-08-463-432B-39
Sequence 39, Application US/08463432B
Patent No. 5786328
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,432B
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-432B-39

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFRAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 56
DB 4 ACNLPVIRGPCRAFIQLMAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 58

RESULT 11

US-08-676-125A-47
; Sequence 47, Application US/08676125A
; Patent No. 5795865
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: KALIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS AND ANALOGUES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESS: Yankwich & Associates
; STREET: 130 Bishop Allen Drive, fifth floor
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word for Windows 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,125A
; FILING DATE: 25 September 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00299
; FILING DATE: 11 January 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,964
; FILING DATE: 11 January 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,264
; FILING DATE: 10 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: DIX-006.2P US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 491-4343
; TELEFAX: (617) 491-8801
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-676-125A-47

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFRAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 56
DB 4 ACNLPVIRGPCRAFIQLMAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 58

RESULT 12

US-08-206-310A-39
; Sequence 39, Application US/08206310A
; Patent No. 5795954

; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ DOMAIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,310A
FILING DATE: 04-Mar-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.

REGISTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER: 882
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1249
TELEFAX: 415/952-9881

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-206-310A-39

Query Match 90.0%; Score 296; DB 1; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFRAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 56
DB 4 ACNLPVIRGPCRAFIQLMAFDVAVKGCVLFPYGGCGGNKNKFSSEKREYCGVP 58

RESULT 13

US-08-398-010A-39
; Sequence 39, Application US/08398010A
; Patent No. 5834244
; GENERAL INFORMATION:
; APPLICANT: Robert A. Lazarus and Mark S. Dennis
; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,010A
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/206310

FILING DATE: 04-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 32,637
 REFERENCE/DOCKET NUMBER: P0882P1-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-398-010A-39

Query Match 90.0%; Score 296; DB 2; Length 58;
 Best Local Similarity 92.7%; Pred. No. 9e-23;
 Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 56
 Db 4 ACNLPYVGPCTIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 58

RESULT 14
 US-08-398-628A-39
 Sequence 39, Application US/08398628A
 Patent No. 5863893

GENERAL INFORMATION:
 APPLICANT: Robert A. Lazarus and Mark S. Dennis
 TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
 TITLE OF INVENTION: DOMAIN PROTEINS
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/398,628A
 FILING DATE: 03-Mar-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/206310
 FILING DATE: 04-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0882P1-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-398-628A-39

Query Match 90.0%; Score 296; DB 2; Length 58;
 Best Local Similarity 92.7%; Pred. No. 9e-23;
 Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 56

Db 4 ACNLPYVGPCTIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 58

RESULT 15
 US-08-399-115A-39
 Sequence 39, Application US/08399115A
 Patent No. 5880256

GENERAL INFORMATION:
 APPLICANT: Robert A. Lazarus and Mark S. Dennis
 TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
 TITLE OF INVENTION: DOMAIN PROTEINS
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/399,115A
 FILING DATE: 03-Mar-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/206310
 FILING DATE: 04-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0882P1-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-399-115A-39

Query Match 90.0%; Score 296; DB 2; Length 58;
 Best Local Similarity 92.7%; Pred. No. 9e-23;
 Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 56
 Db 4 ACNLPYVGPCTIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSKREYCGVP 58

RESULT 16
 US-09-136-012A-47
 Sequence 47, Application US/09136012A
 Patent No. 5994125
 GENERAL INFORMATION:
 APPLICANT: DYAX CORP
 APPLICANT: MARKLAND, William
 APPLICANT: LADNER, Robert Charles
 TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS
 TITLE OF INVENTION: AND ANALOGUES THEREOF
 NUMBER OF SEQUENCES: 73
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Yankwich & Associates
 STREET: 130 Bishop Allen Drive, fifth floor
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: United States of America

ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,012A
FILING DATE: 17-August-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,125
FILING DATE: 25-September-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00299
FILING DATE: 11-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,264
FILING DATE: 10-March-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,964
FILING DATE: 11-January-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R.
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P.
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-006.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 491-4343
TELEFAX: (617) 491-8801
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-012A-47

Query Match 90.0%; Score 296; DB 2; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFRRNAPDAVKGCYLPFYGGCGGNGNKFYSKRECRYGVP 56
DB 4 ACNLPVIRGPCIAFPFRRNAPDAVKGCYLPFYGGCGGNGNKFYSKRECRYGVP 58

RESULT 17
US-08-676-124-78
Sequence 78, Application US/08676124
Patent No. 6010860
GENERAL INFORMATION:
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IYER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND-3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-78

Query Match 90.0%; Score 296; DB 3; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFRRNAPDAVKGCYLPFYGGCGGNGNKFYSKRECRYGVP 56
DB 4 ACNLPVIRGPCIAFPFRRNAPDAVKGCYLPFYGGCGGNGNKFYSKRECRYGVP 58

RESULT 18
US-09-414-878-78
Sequence 78, Application US/09414878
Patent No. 6071723
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plamin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265

FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-78

Query Match 90.0%; Score 296; DB 3; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFPAFPAVKGKCVLPFYGGCGGNGNKFYSKRECYGVP 56
DB 4 ACNLPVIRGPCIAFPFPAFPAVKGKCVLPFYGGCGGNGNKFYSKRECYGVP 58

RESULT 19
US-09-240-136-78
Sequence 78, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kuntz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,136
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237

NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-78

Query Match 90.0%; Score 296; DB 3; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFPFPAFPAVKGKCVLPFYGGCGGNGNKFYSKRECYGVP 56
DB 4 ACNLPVIRGPCIAFPFPAFPAVKGKCVLPFYGGCGGNGNKFYSKRECYGVP 58

RESULT 20
US-09-638-770A-78
Sequence 78, Application US/09638770A
Patent No. 6423498
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kuntz Domains
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,770A
FILING DATE: 15-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-638-770A-78

Query Match 90.0%; Score 296; DB 4; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPGCIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 4 ACNLPVIRGPGCIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 58

RESULT 21

PCT-US92-03132-11
Sequence 11, Application PC/TUS9203132
GENERAL INFORMATION:
APPLICANT: Houston, L. L.
APPLICANT: Liu, David Y.
APPLICANT: Kaymakalan, Zehra
TITLE OF INVENTION: Method for Inhibiting Adhesion of White
TITLE OF INVENTION: Blood Cells to Endothelial Cells
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-Third Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03132
FILING DATE: 19920416
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/700,526
FILING DATE: 14-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 2600.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3217
TELEFAX: (415) 658-5239
TELEX: 4992659
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03132-11

Query Match 90.0%; Score 296; DB 5; Length 58;
Best Local Similarity 92.7%; Pred. No. 9e-23;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPGCIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 2 ACNLPVIRGPGCIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 22
US-07-791-213D-8
Sequence 8, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:

APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshihiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-213D-8

Query Match 90.0%; Score 296; DB 1; Length 66;
Best Local Similarity 92.7%; Pred. No. 1e-22;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 4 ACNLPVIRGPGCIAFPFRMAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 58

RESULT 23
US-08-293-150A-8
Sequence 8, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:

APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshihiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-8

Query Match 90.0%; Score 296; DB 1; Length 66;
Best Local Similarity 92.7%; Pred. No. 1e-22;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACNLPYVGPCTIAFPFPAVDVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 4 ACNLPYVGPCTIAFPFPAVDVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 58

RESULT 24
US-07-972-387-76
Sequence 76, Application US/07972387
Patent No. 5451659
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshinori
APPLICANT: No. 5451659uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,387
FILING DATE: 19921105
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-124P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345

INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..68
OTHER INFORMATION: /label= sequence
US-07-972-387-76

Query Match 90.0%; Score 296; DB 1; Length 68;
Best Local Similarity 92.7%; Pred. No. 1e-22;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 2 ACNLPYVGPCTIAFPFPAVDVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56

RESULT 25
US-08-431-412-76
Sequence 76, Application US/08431412
Patent No. 5589360
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshinori
APPLICANT: No. 5589360uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,412
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/972,387
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-124P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..68
OTHER INFORMATION: /label= sequence

OTHER INFORMATION: /note= "AN68 polypeptide"
US-08-431-412-76

US-08-431-412-76

Query Match	90.0%; Score 296; DB 1; Length 68;
Best Local Similarity	93.7%; Prod No. 10-33;

Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 2 ACNLP IVRGPCRAFIQLWAFDAVKKCVLFPIGGCGNGNKKFYSEKECREYCGVP 56

Search completed: February 23, 2005, 03:30:38
Job time : 25 secs

Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 23, 2005, 03:28:20 ; Search time 183 Seconds

(without alignments)
357.423 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPYIRGPCIAPFPRWA.....QGNNGKFKYSKREYCGVP 56

Scoring table:

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Gapd 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	56	1 PCT-US03-17665-49	Sequence 49, Appl
2	329	100.0	56	12 US-08-849-406-27	Sequence 27, Appl
3	329	100.0	56	12 US-08-849-406A-27	Sequence 27, Appl
4	329	100.0	56	26 US-10-038-722-27	Sequence 27, Appl
5	329	100.0	56	29 US-10-361-997-40	Sequence 40, Appl
6	329	100.0	56	30 US-10-456-986A-49	Sequence 49, Appl
7	329	100.0	56	35 US-10-931-153-23	Sequence 23, Appl
8	329	100.0	141	12 US-08-849-406-74	Sequence 74, Appl
9	329	100.0	141	12 US-08-849-406A-74	Sequence 74, Appl
10	329	100.0	141	26 US-10-038-722-27	Sequence 74, Appl
11	329	100.0	655	29 US-10-361-997-59	Sequence 59, Appl
12	329	100.0	655	29 US-10-361-997-61	Sequence 61, Appl
13	329	100.0	694	29 US-10-361-997-71	Sequence 71, Appl
14	329	100.0	728	29 US-10-361-997-75	Sequence 75, Appl
15	329	100.0	729	29 US-10-361-997-46	Sequence 46, Appl
16	329	100.0	752	29 US-10-361-997-74	Sequence 74, Appl
17	329	100.0	753	29 US-10-361-997-45	Sequence 45, Appl
18	324	98.5	56	1 PCT-US03-17665-47	Sequence 47, Appl
19	324	98.5	56	1 PCT-US03-17665-48	Sequence 48, Appl
20	324	98.5	56	12 US-08-849-406-26	Sequence 26, Appl
21	324	98.5	56	12 US-08-849-406A-26	Sequence 26, Appl
22	324	98.5	56	26 US-10-038-722-26	Sequence 26, Appl
23	324	98.5	56	30 US-10-456-986A-47	Sequence 47, Appl
24	324	98.5	56	30 US-10-456-986A-48	Sequence 48, Appl
25	324	98.5	58	4 US-08-085-126-5	Sequence 5, Appl
26	324	98.5	58	8 US-08-438-114-5	Sequence 5, Appl
27	324	98.5	141	12 US-08-849-406-72	Sequence 72, Appl
28	324	98.5	141	12 US-08-849-406-76	Sequence 76, Appl
29	324	98.5	141	12 US-08-849-406A-72	Sequence 72, Appl
30	324	98.5	141	12 US-08-849-406A-76	Sequence 76, Appl
31	324	98.5	141	26 US-10-038-722-12	Sequence 72, Appl
32	324	98.5	141	26 US-10-038-722-76	Sequence 76, Appl
33	317	96.4	58	4 US-08-085-126-6	Sequence 6, Appl
34	317	96.4	58	8 US-08-438-114-6	Sequence 6, Appl
35	308	93.6	58	4 US-08-085-126-115	Sequence 115, App
36	308	93.6	58	8 US-08-438-114-115	Sequence 115, App
37	296	90.0	56	35 US-10-931-153-12	Sequence 12, Appl
38	296	90.0	57	16 US-09-218-913B-26	Sequence 26, Appl
39	296	90.0	57	16 US-09-218-913D-26	Sequence 26, Appl
40	296	90.0	57	18 US-09-441-966-26	Sequence 26, Appl
41	296	90.0	57	18 US-09-441-966A-26	Sequence 26, Appl
42	296	90.0	57	18 US-09-441-966B-26	Sequence 26, Appl
43	296	90.0	57	25 US-09-974-026-26	Sequence 26, Appl
44	296	90.0	58	1 PCT-US03-17665-31	Sequence 31, Appl
45	296	90.0	58	3 US-07-687-300-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
PCT-US03-17665-49
; Sequence 49, Application PC/TUS0317665
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hiran, Shrish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001004
; CURRENT APPLICATION NUMBER: PCT/US03/17665
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 49
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPI-HNE-4 Sequence
PCT-US03-17665-49

Query Match
Best Local Similarity 100.0%; Score 329; DB 1; Length 56;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKCKREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKCKREYCGVP 56

RESULT 2
US-08-849-406-27
; Sequence 27, Application US/08849406
; APPLICANT: LEY, Arthur C.
; LADNER, Robert C.
; GUTERMAN, Sonia K.
; ROBERTS, Bruce L.
; MARKLAND, William
; KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,406
; FILING DATE: 21-Jul-1999
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16349
; FILING DATE: 15-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-08-849-406-27

Query Match
Best Local Similarity 100.0%; Score 329; DB 12; Length 56;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKCKREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKCKREYCGVP 56
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RESULT 3
US-08-849-406A-27
; Sequence 27, Application US/08849406A
; APPLICANT: LEY, Arthur C.
; LADNER, Robert C.
; GUTERMAN, Sonia K.
; ROBERTS, Bruce L.
; MARKLAND, William
; KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,406A
; FILING DATE: 21-Jul-1999
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16349
; FILING DATE: 15-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-08-849-406A-27

Query Match
Best Local Similarity 100.0%; Score 329; DB 12; Length 56;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKCKREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSKCKREYCGVP 56

RESULT 4
US-10-038-722-27
; Sequence 27, Application US/10038722
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
```

; PRIOR FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: PCT/US95/16349
 ; PRIOR FILING DATE: 1995-12-15
 ; PRIOR APPLICATION NUMBER: US 08/358,160
 ; PRIOR FILING DATE: 1994-12-16
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Epi-HNE-4
 US-10-038-722-27

Query Match 100.0%; Score 329; DB 26; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
 DB 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

RESULT 5
 US-10-361-997-40
 ; Sequence 40, Application US/10361997
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert Charles
 ; APPLICANT: Ley, Arthur C.
 ; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
 ; FILE REFERENCE: 3421,1015-000
 ; CURRENT APPLICATION NUMBER: US/10/361,997
 ; CURRENT FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: US 60/355,547
 ; PRIOR FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Polypeptide sequence
 US-10-361-997-40

Query Match 100.0%; Score 329; DB 29; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
 DB 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

RESULT 6
 US-10-456-986A-49
 ; Sequence 49, Application US/10456986A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Ley, Arthur C.
 ; APPLICANT: Hiran, Shriah
 ; APPLICANT: Williams, Anthony
 ; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
 ; FILE REFERENCE: 3421,1001-002
 ; CURRENT APPLICATION NUMBER: US/10/456,986A
 ; CURRENT FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: 60/387,239
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: 60/407,003
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: EPI-HNE-4 Sequence
 US-10-456-986A-49

Query Match 100.0%; Score 329; DB 30; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
 DB 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

RESULT 7
 US-10-931-153-23
 ; Sequence 23, Application US/10931153
 ; GENERAL INFORMATION:
 ; APPLICANT: Ley, Arthur C.
 ; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Stochl, Mark
 ; TITLE OF INVENTION: POLY-PREGYLATED PROTEASE INHIBITORS
 ; FILE REFERENCE: 10280-119001
 ; CURRENT APPLICATION NUMBER: US/10/931,153
 ; CURRENT FILING DATE: 2004-08-30
 ; PRIOR APPLICATION NUMBER: US 60/498,845
 ; PRIOR FILING DATE: 2003-08-29
 ; PRIOR APPLICATION NUMBER: US 60/598,967
 ; PRIOR FILING DATE: 2004-08-04
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 56
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated peptide
 US-10-931-153-23

Query Match 100.0%; Score 329; DB 35; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
 DB 1 EACNLPVIRGPCIAFFPRMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

RESULT 8
 US-08-849-406-74
 ; Sequence 74, Application US/08849406
 ; APPLICANT: Ley, Arthur C.
 ; APPLICANT: LADNER, Robert C.
 ; APPLICANT: GUTERMAN, Sonia K.
 ; APPLICANT: ROBERTS, Bruce L.
 ; APPLICANT: MARKLAND, William
 ; APPLICANT: KENT, Rachel B.
 ; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
 ; DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 ; STREET: 624 Ninth Street, N.W. Suite 300
 ; CITY: Washington
 ; STATE: District of Columbia
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-08-849-406-74

Query Match
Best Local Similarity 100.0%; Score 329; DB 12; Length 141;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EACNLPYVGPICIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56
86 EACNLPYVGPICIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 141

RESULT 9
US-08-849-406A-74
; Sequence 74, Application US/08849406A
; APPLICANT: LEY, Arthur C.
; LADNER, Robert C.
; GUTERMAN, Sonia K.
; ROBERTS, Bruce L.
; MARKLAND, William
; KENT, Rachel B.
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,406A
; FILING DATE: 21-Jul-1999
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16349
; FILING DATE: 15-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-08-849-406A-74

Query Match
Best Local Similarity 100.0%; Score 329; DB 12; Length 141;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EACNLPYVGPICIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56
86 EACNLPYVGPICIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 141

RESULT 10
US-10-038-722-74
; Sequence 74, Application US/10038722
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 74
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BacBI-AatII-EcoRI cassette for expression of Epi-HNE-4 (Table 252
; OTHER INFORMATION:)
US-10-038-722-74

Query Match
Best Local Similarity 100.0%; Score 329; DB 26; Length 141;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EACNLPYVGPICIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 56
86 EACNLPYVGPICIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFKYSEKREYCGVP 141

RESULT 11
US-10-361-997-59
; Sequence 59, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84


```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the N-terminal
; OTHER INFORMATION: DX-890-(GGG)4GG-albumin fusion protein
US-10-361-997-59

```

```

Query Match          100.0%; Score 329; DB 29; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.2e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
Db      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

```

```

RESULT 12
US-10-361-997-61
; Sequence 61, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the C-terminal
; OTHER INFORMATION: albumin-(GGG)4GG-DX-890 fusion protein
US-10-361-997-61

```

```

Query Match          100.0%; Score 329; DB 29; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.2e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
Db      600 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 655

```

```

Query Match          100.0%; Score 329; DB 29; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.2e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
Db      600 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 655

```

```

RESULT 13
US-10-361-997-71
; Sequence 71, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence encoded by NotI cassette of
; OTHER INFORMATION: pDB2300X2 with DX890 (Nterm) and Cterm linker
; OTHER INFORMATION: ready for second DX890

```

```

Qy      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
Db      674 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 729

```

```

US-10-361-997-71

```

```

Query Match          100.0%; Score 329; DB 29; Length 694;
Best Local Similarity 100.0%; Pred. No. 2.3e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
Db      25 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 80

```

```

RESULT 14
US-10-361-997-75
; Sequence 75, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of
; OTHER INFORMATION: DX-890::(GGG)4GG::HA::(GGG)4GG::DX890
US-10-361-997-75

```

```

Query Match          100.0%; Score 329; DB 29; Length 728;
Best Local Similarity 100.0%; Pred. No. 2.4e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
Db      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56

```

```

RESULT 15
US-10-361-997-46
; Sequence 46, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Secreted product
US-10-361-997-46

```

```

Query Match          100.0%; Score 329; DB 29; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.4e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 51; Gaps 0;

```

```

Qy      1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 56
Db      674 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCCGNGNKFYSEKCREYCGVP 729

```

Thu Feb 24 06:30:13 2005

us-10-038-722-27.rapm

Page 6

Search completed: February 23, 2005, 03:34:59
Job time : 185 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 23, 2005, 03:10:59 ; Search time 23 Seconds
(without alignments)
234.267 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPYVRGPCIAPFFPRWA.....QGNNGKFXSEKREYCGVP 56

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	296	90.0	352	1	HCHU
2	272	82.7	337	1	TIHGBI
3	269	81.8	352	1	TIHOB1
4	264	80.2	125	1	TIHOB1
5	261	79.3	349	2	S35708
6	258	78.4	349	2	S21089
7	257	78.1	123	2	A29652
8	155	47.1	111	2	S41082
9	155	47.1	751	2	A49321
10	155	47.1	763	2	A49321
11	155	47.1	765	2	S42880
12	154	46.8	252	2	JG0185
13	152	46.2	355	1	S22181
14	151	45.9	62	2	S07451
15	150	45.6	76	2	S04855
16	150	45.6	100	2	A32282
17	148	45.0	64	2	S41399
18	146	44.4	76	2	S06678
19	146	44.4	76	2	S03607
20	146	44.4	484	4	A32761
21	146	44.4	770	1	QRHUA4
22	146	44.4	2225	2	T26063
23	144	43.8	922	2	T23573
24	140	42.6	55	2	S30332
25	138	41.9	61	1	TIWITI
26	138	41.9	747	2	JH0773
27	138	41.9	2167	2	T34395
28	136	41.3	61	1	TIHCBP
29	135	41.0	56	2	JN0380

30	135	41.0	65	1	TIWIVC	venom basic protei
31	134	40.7	1558	2	C89114	protein C37C3.6a f
32	133	40.4	57	2	B59399	short epsilon-dend
33	133	40.4	59	1	TIHPRD	venom basic protei
34	133	40.4	59	2	A59399	Long epsilon-dendr
35	133	40.4	122	1	A55115	uterine plasmin/cr
36	133	40.4	3176	2	CGHUA3	collagen alpha 3(V
37	132	40.1	58	1	TIHABK	isoinhibitor K (BP
38	132	40.1	372	2	JC2556	alpha-1-microglobu
39	129	39.2	235	2	A54951	tissue factor path
40	129	39.2	299	2	I46937	tissue factor path
41	129	39.2	300	2	S12143	lipoprotein-associ
42	128	38.9	67	1	TIHBOC	trypsin inhibitor,
43	127	38.6	63	1	TIHFAV	acrosin inhibitor
44	126	38.3	57	1	TIHFAV	venom basic protei
45	126	38.3	62	2	A44180	taicatoxin serine

ALIGNMENTS

RESULT 1

HCHU
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human
N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) pr
rich protein
M:Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1982 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; P0450; B39079; A61580; B25
3217
R:Vetr, H.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
A:Reference number: S13433; MUID:91214554; PMID:1708673
A:Accession: S13433
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <VENT>
A:Cross-references: UNIPROT:P02760; EMBL:X54816; NID:G24475; PIDN:CAA38585.1; PID:G82561
R:Diatra-Mehrpour, M.; Bourguignon, J.; Seebouee, R.; Sallier, J.P.; Leveillard, T.; Mart
Eur. J. Biochem. 191, 131-139, 1990
A:Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
A:Reference number: S10778; MUID:90336621; PMID:1696200
A:Accession: S10778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <DIA>
A:Residues: 1-202 <DIA>
R:Kaumeyer, J.F.; Polazzi, J.O.; Kotlick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A:Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-
A:Reference number: A93642; MUID:87040757; PMID:2430261
A:Accession: A93642
A:Molecule type: mRNA
A:Residues: 1-352 <KAB>
A:Cross-references: GB:X04494; NID:G24478; PIDN:CAA28182.1; PID:G24479
R:Lopez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A:Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge
A:Reference number: A90074; MUID:84126849; PMID:6198962
A:Accession: A90074
A:Molecule type: protein
A:Residues: 20-56,58-202 <LOP>
A:Experimental source: individual with tubular proteinuria
A>Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
R:Takagi, T.; Takagi, K.; Kawai, T.
Biochem. Biophys. Res. Commun. 98, 997-1001, 1991
A:Title: Complete amino acid sequence of human alpha-1-microglobulin.
A:Reference number: A90225; MUID:81184038; PMID:6164372
A:Accession: A90225
A:Molecule type: protein
A:Residues: 20-47,58-136,138-141, 'T', 143-144, 146-198 <TAK>
A:Experimental source: pooled urine of patients with tubular proteinuria

R.Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempart, K.; Sallier, J.P.
 Biol. Chem. Hoppe-Seyler 366, 479-483, 1995
 A>Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
 A:Reference number: A50686; PMID:8522568; PMID:2408638
 A:Accession: A50686
 A:Molecule type: protein
 A:Residues: 206-290, 'YI', 293-342, 'E', 344-350 <RE1>
 R.Altman, F.; Lacom, B.; Strecker, P.; Parvy, P.; Drueke, T.; Daudon, M.
 Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
 A>Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca
 A:Reference number: PNO450; PMID:93221481; PMID:8466493
 A:Accession: PNO450
 A:Molecule type: protein
 A:Residues: 206-214, 'X', <ATM1>
 R.Englund, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
 J. Biol. Chem. 266, 747-751, 1991
 A>Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
 A:Reference number: B39079; PMID:91093267; PMID:1898736
 A:Accession: B39079
 A:Molecule type: protein
 A:Residues: 206-225 <ENG1>
 R.Chiriac, F.; Baldyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
 Int. J. Biochem. 23, 1201-1203, 1991
 A>Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inhi
 A:Reference number: A61580; PMID:92175157; PMID:1794445
 A:Accession: A61580
 A:Molecule type: protein
 A:Residues: 214, 'X', 216-222, 'X', <CH1>
 R.McKeenan, W.L.; Sakagami, Y.; Hostin, H.; McKeenan, K.A.
 J. Biol. Chem. 261, 5378-5383, 1986
 A>Title: Two apparent human endocytelial cell growth factors from human hepatoma cells ar
 A:Reference number: A92583; PMID:86168278; PMID:3007499
 A:Accession: B25604
 A:Molecule type: protein
 A:Residues: 206-218, 'X', 216-230, 'X', 232-239, 'X', 241-248, 'XX', 251-252, 'X', 254 <MCK>
 R.Englund, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
 J. Biol. Chem. 264, 15975-15981, 1989
 A>Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-a
 A:Reference number: A92736; PMID:89380192; PMID:2476436
 A:Accession: C34245
 A:Molecule type: protein
 A:Residues: 206-225 <ENG2>
 R.Tiraboni, C.; Cortese, R.
 Nucleic Acids Res. 14, 6340, 1986
 A>Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobu
 A:Reference number: A25303; PMID:86312901; PMID:2428011
 A:Accession: A25303
 A:Molecule type: mRNA
 A:Residues: 1-218, 'HW', <TRA>
 A>Note: this mRNA sequence appears to contain errors after residue 218
 R.Calero, M.; Escridano, J.; Grubb, A.; Mendez, E.
 J. Biol. Chem. 269, 384-389, 1994
 A>Title: Location of a novel type of interpolyptide chain linkage in the human protei
 A:Reference number: A53110; PMID:94103241; PMID:7506257
 A:Accession: A53110
 A:Molecule type: protein
 A:Residues: 45-57 <CAL1>
 R.Verr, H.; Kogler, M.; Gebhard, W.
 FEBS Lett. 245, 137-140, 1989
 A>Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inhi
 A:Reference number: S03552; PMID:89171290; PMID:2466696
 A:Accession: S03552
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 206-352 <VET2>
 R.Malki, N.; Baldyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartat, A.; Fourn
 Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
 A>Title: The heavy chain of human plasma inter-alpha-trypsin inhibitor: their isolation
 A:Reference number: S28928; PMID:93039735; PMID:1384548
 A:Accession: S28930
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-215 <ML>

R.Morelle, W.; Capon, C.; Baldyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Fourn
 Eur. J. Biochem. 221, 881-888, 1994
 A>Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of int
 A:Reference number: S43466; PMID:94229087; PMID:7533643
 A:Accession: S43466
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-221 <MOR>
 R.Miniowski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
 Biochemistry 33, 7423-7429, 1994
 A>Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp
 A:Reference number: A53642; PMID:94271799; PMID:7516184
 A:Accession: A53642
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-217 <MIS>
 R.Calero, M.; Mendez, E.; Garcia, E.
 Biochem. Biophys. Acta 1249, 91-99, 1995
 A>Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
 A:Reference number: S55688; PMID:95284116; PMID:7539295
 A:Accession: S55688
 A:Molecule type: protein
 A:Residues: 20-24 <CH2>
 R.Bourguignon, J.; Diarra-Mehrpour, M.; Sebboue, R.; Frain, M.; Sala-Trepat, J.M.; Marti
 Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
 A>Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide se
 A:Reference number: I52208; PMID:86025577; PMID:2413856
 A:Accession: I52208
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 302-352 <BOU>
 A:Cross-references: GB:M1562; NID:G186587; PIDN:AAA59194.1; PID:G307077
 R.Mojcik, E.G.C.; Van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Berti
 Biochem. J. 311, 753-759, 1995
 A>Title: Factor IX zutphen: a Cys(18) -> Arg mutation results in formation of a heterodi
 A:Reference number: S59509; PMID:96067589; PMID:7487923
 A:Accession: S59509
 A:Molecule type: protein
 A:Residues: 27-35, 'Y', 37 <MOJ>
 R.Altman, F.; Mizon, J.; Khan, S.R.
 Eur. J. Biochem. 236, 984-990, 1996
 A>Title: Identification of uronic-acid-rich protein as urinary bikunin, the light chain
 A:Reference number: S66434; PMID:96270753; PMID:8665922
 A:Accession: S66434
 A:Molecule type: protein
 A:Residues: 206-214, 'X', 216-230 <ATM2>
 R.Akerstrom, B.; Bratt, T.; Englund, J.J.
 FEBS Lett. 362, 50-54, 1995
 A>Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect cel
 A:Reference number: S68728; PMID:95212582; PMID:7535251
 A:Accession: S68728
 A:Molecule type: protein
 A:Residues: 89-100 <AKS>
 R.Jessen, T.E.; Faarvang, K.L.; Ploug, M.
 FEBS Lett. 230, 195-200, 1988
 A>Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a nc
 A:Reference number: S02431; PMID:88167187; PMID:2450785
 A:Accession: S02431
 A:Molecule type: protein
 A:Residues: 206-214, 'X', 216-217 <JES>
 R.Lopez, C.; Grubb, A.; Mendez, E.
 FEBS Lett. 144, 349-353, 1982
 A>Title: Human protein HC displays variability in its carboxyl-terminal amino acid sequ
 A:Reference number: A91304
 A:Contents: annotation; variant of alpha-1-microglobulin
 A>Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys an
 R.Hochstrasser, K.; Schobberger, O.L.; Rosenblatt, I.; Wachter, E.
 Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
 A>Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
 A:Reference number: A51698; PMID:82074265; PMID:6171497
 A:Contents: annotation; carbohydrate binding sites
 R.Moril, M.; Travis, J.

Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
 A:Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-terminal
 A:Reference number: A90682; MUID:85225940; PMID:3890890
 A:Contents: annotation: inhibitory site
 A>Note: in vitro, the first twelve residues of the amino end of the inhibitor appear to

Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolytically
 C:Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma, u
 It contains at least one brown-yellow chromophore.

Query Match 90.0%; Score 296; DB 1; Length 352;
 Best Local Similarity 92.7%; Pred. No. 3.3e-28;
 Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGGPCIAFPFPAWDAVKGKCVLPYGGCGGNGKPKYSEKREYCGVP 56
 Db 286 ACNLPYVGGPCIAFPFPAWDAVKGKCVLPYGGCGGNGKPKYSEKREYCGVP 340

RESULT 2

TIPOBI

alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
 N:Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 30-Jun-1987 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: S11066; S13493; A01208

R:Gehard, W.; Schrettmüller, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.

FEBS Lett. 269, 32-36, 1990

A:Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microglobu

A:Reference number: S11066; MUID:90353595; PMID:1696914

A:Accession: S11066

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-337 <GER>

A:Cross-references: UNIPROT:P04366; EMBL:X53685; NID:91877; PIDN:CAA37725.1; PID:91878

R:Avakol, A.

Biochim. Biophys. Acta 1088, 47-56, 1991

A:Title: Molecular cloning of porcine alpha(1)-microglobulin/HI-30 reveals developmental

A:Reference number: S13493; MUID:91113729; PMID:1703444

A:Accession: S13493

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 'M', 3-48, 'M', 50-337 <TAV>

A:Cross-references: GB:X52087; NID:91881; PIDN:CAA3306.1; PID:91882

A>Note: the authors translated the codon GTG for residue 2 as a Met initiation codon

R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.

Biol. Chem. Hoppe-Seyler 366, 473-478, 1985

A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a

A:Reference number: A90685; MUID:85225967; PMID:2408637

A:Accession: A01208

A:Molecule type: protein

A:Residues: 212-258, 'Q', 260-269, 'S', 271-277, 'Q', 279-282, 'A', 284, 'IR', 287-292, 'A', 294-310

C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis

first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea

C:Comment: The amino acid at position P2' (228-Met) appears to determine the specificity

nd elastase; those with leucine interact strongly.

C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu

C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor

F:20-173/Domain: lipocalin homology <LIP>

F:216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>

F:212-232/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F:216-266, 225-249, 241-262, 272-322, 281-305, 297-318/Disulfide bonds: #status predicted

F:226/inhibitory site: leu (chymotrypsin, elastase) #status predicted

F:235/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:232/inhibitory site: Arg (trypsin) #status predicted

Query Match 82.7%; Score 272; DB 1; Length 337;
 Best Local Similarity 82.1%; Pred. No. 2.5e-25;
 Matches 46; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EACNLPYVGGPCIAFPFPAWDAVKGKCVLPYGGCGGNGKPKYSEKREYCGVP 56
 Db 270 EACNLPYVGGPCIAFPFPAWDAVKGKCVLPYGGCGGNGKPKYSEKREYCGVP 325

RESULT 3

TIPOBI

alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor (validated) - bovine

N:Alternate names: BI-14 (inhibitory fragment of ITI); bikunin; ITI

C:Species: Bos primigenius taurus (cattle)

C:Date: 25-Feb-1985 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: S68149; A91717; A90685; S31219; A01209

R:Andqvist, A.; Akerstrom, B.

Biochim. Biophys. Acta 1306, 98-106, 1996

A:Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver

A:Reference number: S68149; MUID:96201710; PMID:8611630

A:Accession: S68149

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-352 <LIN>

A:Cross-references: UNIPROT:P00978; EMBL:U35642; NID:91016297; PIDN:AAB07599.1; PID:9101

R:Hochstrasser, K.; Wachter, E.

Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983

A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a

A:Reference number: A91717; MUID:84133807; PMID:6199275

A:Accession: A91717

A:Molecule type: protein

A:Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AF', 300-329, 'Q', 331-345, 'R', 347-348 <HOC>

R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.

Biol. Chem. Hoppe-Seyler 366, 473-478, 1985

A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a

A:Reference number: A90685; MUID:85225967; PMID:2408637

A:Accession: A90685

A:Molecule type: protein

A:Residues: 347-349 <HOC>

R:Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.

Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983

A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a

A:Reference number: A91718; MUID:84133808; PMID:6199276

A:Contents: annotation; reactive sites

R:Castillo, G.M.; Templeton, D.M.

FEBS Lett. 318, 292-296, 1993

A:Title: Subunit structure of bovine ERF (extracellular-matrix stabilizing factor(s)). A

A:Reference number: S31219; MUID:93178646; PMID:7680011

A:Accession: S31219

A:Status: preliminary

A:Molecule type: protein

A:Residues: 206-214, 'X', 216, 'X', 218-220 <CAS>

C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu

C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor

F:35-188/Domain: lipocalin homology <LIP>

F:231-281/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>

F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F:241/inhibitory site: leu (chymotrypsin, elastase) #status experimental

F:250/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:297/inhibitory site: Arg (trypsin) #status experimental

Query Match 81.8%; Score 269; DB 1; Length 352;
 Best Local Similarity 78.6%; Pred. No. 6e-25;
 Matches 44; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EACNLPYVGGPCIAFPFPAWDAVKGKCVLPYGGCGGNGKPKYSEKREYCGVP 56
 Db 285 EACNLPYVGGPCIAFPFPAWDAVKGKCVLPYGGCGGNGKPKYSEKREYCGVP 340

RESULT 4

TIPOBI

alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)

N:Alternate names: BI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI

C:Species: Equus caballus (domestic horse)

C:Date: 30-Jun-1987 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: A01210; A45653

R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.

Biol. Chem. Hoppe-Seyler 366, 473-478, 1985

A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a

A:Reference number: A90685; MUID:85225967; PMID:2408637
 A:Accession: A01210
 A:Molecule type: protein
 A:Residues: 3-125 <HOC>
 A:Cross-references: UNIPROT:P04365
 R:Veeragavan, K.; Singu, K.; Wachter, E.; Hochstrasser, K.
 Biochem. Int. 26, 405-413, 1992
 A:Title: Characterization of a trypsin inhibitor from equine urine.
 A:Reference number: A45653; MUID:92328813; PMID:1627153
 A:Accession: A45653
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12, 'E', '14-33 <VE>
 A:Cross-references: PIDN:AB22430.1; PID:9250858
 A:Experimental source: urine
 A:Note: sequence extracted from NCBI backbone (NCBI:P107966)
 C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
 C:Comment: The amino acid at position P2' (19-Met) appears to determine the specificity
 d elastase; those with leucine interact strongly.
 C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
 C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
 F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
 F:17/inhibitory site: leu (chymotrypsin, elastase) #status predicted
 F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:73/inhibitory site: Arg (trypsin) #status predicted

Query Match 80.2%; Score 264; DB 1; Length 135;
 Best Local Similarity 78.2%; Pred. No. 9, 5e-25;
 Matches 43; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCIAFPFPAVAVKGCVLFPYGGCGGNGKNGFYSEKREYCGVP 56
 DB 62 ACNLPYVGPCIAFPFPAVAVKGCVLFPYGGCGGNGKNGFYSEKREYCGVP 116

RESULT 5
 S35708
 alpha-1-microglobulin / bikunin precursor - mouse
 N:Alternate names: alpha 1-microglobulin / inter-alpha-trypsin inhibitor light chain
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S35708; MUID:93363639; PMID:7689339
 R:Chan, P.; Salier, J.P.
 Biochim. Biophys. Acta 1174, 195-200, 1993
 A:Title: Mouse alpha-1-microglobulin/bikunin precursor: cDNA analysis, gene evolution an
 A:Reference number: S35708; MUID:93363639; PMID:7689339
 A:Accession: S35708
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-349 <CHA>
 A:Cross-references: UNIPROT:O07456; EMBL:X68680; NID:g311702; PIDN:CAA48640.1; PID:g3117
 R:Itch, H.; Ide, H.; Kataoka, H.; Tomita, M.; Yoshinara, H.; Nawa, Y.
 J. Biochem. 116, 767-772, 1994
 A:Title: cDNA sequencing of mouse alpha1-microglobulin/inter-alpha-trypsin inhibitor lig
 A:Reference number: JX0355; MUID:95189774; PMID:7533761
 A:Accession: JX0355
 A:Molecule type: mRNA
 A:Residues: 1-64, 'S', '66-349 <ITO>
 A:Cross-references: DBJ:D28812; NID:g556530; PIDN:BA05973.1; PID:g556531
 A:Experimental source: liver
 C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
 C:Keywords: glycoprotein; inflammation; serine proteinase inhibitor
 F:34-187/Domain: lipocalin homology <LIP>
 F:230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:286-336/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:114,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.3%; Score 261; DB 2; Length 349;
 Best Local Similarity 78.2%; Pred. No. 5, 6e-24;
 Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCIAFPFPAVAVKGCVLFPYGGCGGNGKNGFYSEKREYCGVP 56
 DB 285 ACNLPYVGPCIAFPFPAVAVKGCVLFPYGGCGGNGKNGFYSEKREYCGVP 339

RESULT 6
 S21089
 alpha-1-microglobulin/inter-alpha-trypsin inhibitor light chain precursor - rat
 N:Alternate names: acid-stable proteinase inhibitor; bikunin; tryptacin
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S21089; A53056; A25935; A31890; A61633
 R:Lindqvist, A.; Bratt, T.; Altieri, M.; Kaström, W.; Åkerström, B.
 Biochim. Biophys. Acta 1130, 63-67, 1992
 A:Title: Rat alpha(1)-microglobulin: co-expression in liver with the light chain of inte
 A:Reference number: S21089; MUID:92182014; PMID:1371936
 A:Accession: S21089
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-349 <LIN>
 A:Cross-references: UNIPROT:O64240; GB:S87544; NID:g247162; PIDN:AB21782.1; PID:g247163
 R:Itch, H.; Ide, H.; Ishikawa, N.; Nawa, Y.
 J. Biol. Chem. 269, 3818-3822, 1994
 A:Title: Mast cell protease inhibitor, tryptacin, is a fragment of inter-alpha-trypsin
 A:Reference number: A53056; MUID:94148892; PMID:7508921
 A:Accession: A53056
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 285-341 <ITO>
 R:Kaström, W.; Björck, L.; Åkerström, B.
 J. Biol. Chem. 261, 15070-15074, 1986
 A:Title: Developmental and tissue-specific expression of alpha-1-microglobulin mRNA in t
 A:Reference number: A25935; MUID:87033744; PMID:2429963
 A:Accession: A25935
 A:Molecule type: protein
 A:Residues: 141, 'A', '143-195 <KAS>
 R:Kido, H.; Yokogoshi, Y.; Katunuma, N.
 J. Biol. Chem. 263, 18104-18107, 1988
 A:Title: Kunitz-type protease inhibitor found in rat mast cells. Purification, propertie
 A:Reference number: A31890; MUID:89053978; PMID:3263966
 A:Accession: A31890
 A:Molecule type: protein
 A:Residues: 283-301, 'L', '303-322, 'N', '324-329, 'PK', '332-333, 'W', '335-343 <KID>
 R:Suzuki, M.; Maruyama, M.; Yoshida, E.; Sumi, H.; Mihara, H.
 Inflammation 15, 281-289, 1991
 A:Title: Acid-stable protease inhibitor in chronic phase of carrageenin-induced inflamma
 A:Reference number: A61633; MUID:92120777; PMID:1769732
 A:Accession: A61633
 A:Molecule type: protein
 A:Residues: 205-213, 'X', '215-229, 'N', '231-232, 'K', '234-238 <SUG>
 C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
 C:Keywords: chondroitin sulfate proteoglycan; chromoprotein; glycoprotein; plasma; serin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-202/Product: alpha-1-microglobulin #status predicted <AIM>
 F:34-187/Domain: lipocalin homology <LIP>
 F:205-349/Product: inter-alpha-trypsin inhibitor #status experimental <IAI>
 F:230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:286-336/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:24/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F:52/Cross-link: alpha-1-microglobulin-Ig alpha complex chromophore (Cys) (interchain to
 F:114,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:214/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
 F:296/inhibitory site: Arg (trypsin) #status predicted

Query Match 78.4%; Score 258; DB 2; Length 349;
 Best Local Similarity 78.2%; Pred. No. 1, 3e-23;
 Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCIAFPFPAVAVKGCVLFPYGGCGGNGKNGFYSEKREYCGVP 56
 DB 285 ACNLPYVGPCIAFPFPAVAVKGCVLFPYGGCGGNGKNGFYSEKREYCGVP 339

RESULT 7
A29652
inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29652
R/Raad, G.; Hochstrasser, K.; Machter, E.; Reisinger, P.W.M.
Biol. Chem. Hoppe-Seyler 368, 727-731, 1987
A/Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha
sin inhibitor, XI.
A/Reference number: A29652; MUID:87299012; PMID:2441725
A/Accession: A29652
A/Molecule type: protein
A/Residues: 1-123 <RAS>
A/Cross-references: UNIPROT:P13371
C/Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C/Keywords: serine proteinase inhibitor
F/5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F/61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match 78.1%; Score 257; DB 2; Length 123;
Best Local Similarity 76.8%; Pred. No. 6.6e-24;
Matches 43; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 1 EACNLPYRGPCIAFFPRMAFDVAVKGCYVLPYGGCGGNGNKFYSEKREYCYC 56
Db 59 QACNLPYRGPCRAIEIMAFDAVAKGCYVFIYGGCGGNGNPFYQKECKEYCGIP 114

RESULT 8
S41082
amyloid precursor protein homolog - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C/Accession: S41082
R/Petersen, L.C.; Bjorn, S.E.; Norris, F.; Sprecher, C.; Foster, D.C.
FEBS Lett. 338, 53-57, 1994
A/Title: Expression, purification and characterization of a Kunitz-type protease inhibit
A/Reference number: S41082; MUID:94139895; PMID:8307156
A/Accession: S41082
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-111 <PBT>
A/Cross-references: UNIPROT:Q7MAL3
F/59-109/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.1%; Score 155; DB 2; Length 111;
Best Local Similarity 54.9%; Pred. No. 1.3e-11;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Oy 3 CNLPYRGPCIAFFPRMAFDVAVKGCYVLPYGGCGGNGNKFYSEKREYCYC 53
Db 59 CSQEAHTGPCRAVMPRWYFDLSKGCYVFIYGGCGGNNFSESDYCNVAVC 109

RESULT 9
A49974
beta-amyloid precursor protein 2 homolog APLP2 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A49974
R/Stunt, H.H.; Thirakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A/Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
A/Reference number: A49974; MUID:94132029; PMID:8300594
A/Accession: A49974
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-751 <SLD>
A/Cross-references: UNIPROT:Q60709; GB:U15571; NID:G558467; PIDN:AAA50603.1; PID:G558468
A/Note: sequence extracted from NCBI backbone (NCBIP:144636)
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

F/310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.1%; Score 155; DB 2; Length 751;
Best Local Similarity 54.9%; Pred. No. 7.4e-11;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Oy 3 CNLPYRGPCIAFFPRMAFDVAVKGCYVLPYGGCGGNGNKFYSEKREYCYC 53
Db 310 CSQEAHTGPCRAVMPRWYFDLSKGCYVFIYGGCGGNNFSESDYCNVAVC 360

RESULT 10
A49321
amyloid beta (A4) homolog 2 precursor - human
N/Alternate names: CDBI-binding protein
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A49321; S34644; S40519
R/Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Foster,
Biochemistry 32, 4481-4486, 1993
A/Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
A/Reference number: A49321; MUID:93250009; PMID:8485127
A/Accession: A49321
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-763 <SPR>
A/Cross-references: UNIPROT:Q06481; GB:S60099; NID:G300168; PIDN:AAC60589.1; PID:G300169
A/Experimental source: placenta
A/Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)
A/Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R/von der Kammer, H.; Klaunder, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A/Description: The human homologue of the murine CDBI binding protein is an amyloid prec
A/Reference number: S34644
A/Accession: S34644
A/Molecule type: mRNA
A/Residues: 1-763 <VOM>
A/Cross-references: EMBL:Z22572; NID:G394763; PIDN:CAA80295.1; PID:G394764
R/Masco, W.; Gurnahagavatu, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A/Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A/Reference number: S40519; MUID:94035131; PMID:8220435
A/Accession: S40519
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-763 <MAS>
A/Cross-references: GB:L27631; NID:G450391; PIDN:AAC41701.1; PID:G450392
A/Genetics:
C/Genetics:
A/Map position: 11q23-11q25
A/Cross-references: GDB:139159; OMIM:104776
A/Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precurs

A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAS>
A:Cross-references: UNIPROT:P15943; EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein prec
A:Reference number: S47528; MUID:94368849; PMID:8086458
A:Accession: S47528
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SAS>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing
F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.1%; Score 155; DB 2; Length 765;
Best Local Similarity 54.9%; Pred. No. 7.6e-11;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Qy 3 CNLPVIRGPCIAFFPRMAFDVAVKGVLPFYGGCGGNGNKFYSEKRECYG 53
Db 312 CSQAMTGPCRAVMPRWYFDLSKGCVRFYGGCGGNNRNFSESDYCMAYC 362

RESULT 12

hepatocyte growth factor activator inhibitor type 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 15-Mar-2004
A:Accession: JG0185
R:Itch, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Kono, M.
Biochem. Biophys. Res. Commun. 255, 740-748, 1999
A:Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz-ty
A:Reference number: JG0185; MUID:99160423; PMID:10049781
A:Accession: JG0185
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-252 <ITO>
A:Cross-references: GB:AFO99016
F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.8%; Score 154; DB 2; Length 252;
Best Local Similarity 47.2%; Pred. No. 3.6e-11;
Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 1 EACNLPVIRGPCIAFFPRMAFDVAVKGVLPFYGGCGGNGNKFYSEKRECYG 53
Db 131 EYCVKAVTGPCRAVMPRWYDTEKNSCTSFYGGCGGNGNKSYLEQACMCHC 183

RESULT 13

gamma-1-microglobulin precursor - plaice
C:Species: Pleuronectes platessa (plaice)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: S22181
R:Leaver, M.J.
submitted to the EMBL Data Library, December 1991
A:Reference number: S22181
A:Accession: S22181
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <LEA>
A:Cross-references: UNIPROT:P36992; EMBL:X63762; NID:964233; PIDN:CAA5294.1; PID:964234
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
F:37-189/Domain: lipocalin homology <LIP>
F:236-286/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:292-342/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.2%; Score 152; DB 1; Length 355;

Best Local Similarity 50.9%; Pred. No. 8.7e-11;
Matches 27; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 3 CNLPVIRGPCIAFFPRMAFDVAVKGVLPFYGGCGGNGNKFYSEKRECYG 55
Db 292 CRLPMAPEPTGPTTMAFDVTSVCMPTGKDGICQANNOFYSRAECQYGV 344

RESULT 14

proteinase inhibitor 5.11 - snake-locks sea anemone
C:Species: Anemonia sulcata (snake-locks sea anemone)
C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
A:Accession: S07451; B27222
R:Munderer, G.; Machleidt, W.; Fritz, H.
Meth. Enzymol. 80, 816-820, 1981
A:Title: The broad-specificity proteinase inhibitor 5.11 from the sea anemone Anemonia s
A:Reference number: S07451
A:Accession: S07451
A:Molecule type: protein
A:Residues: 1-59 <WUN>
A:Cross-references: UNIPROT:P10280
A:Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R:Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A:Title: Isolierung und strukturelle Klärung eines haemolytisch aktiven peptids aus der s
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 45.9%; Score 151; DB 2; Length 62;
Best Local Similarity 49.1%; Pred. No. 2.3e-11;
Matches 26; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 3 CNLPVIRGPCIAFFPRMAFDVAVKGVLPFYGGCGGNGNKFYSEKRECYG 55
Db 5 CELPVVGPCCRAVMPRWYFDLSKGCVRFYGGCGGNNRNFSESDYCMAYC 57

RESULT 15

Alzheimer's disease amyloid A4 protein - mouse (fragment)
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
A:Accession: S04855
R:Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
Nucleic Acids Res. 17, 5396, 1989
A:Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor o
A:Reference number: S04855; MUID:89345111; PMID:2569770
A:Accession: S04855
A:Molecule type: mRNA
A:Residues: 1-76 <FUK>
A:Cross-references: UNIPROT:P12023; EMBL:X15210; NID:949965; PIDN:CAA33280.1; PID:993013
C:Note: the authors translated the codon GAR for residue 74 as Val
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 45.6%; Score 150; DB 2; Length 76;
Best Local Similarity 50.0%; Pred. No. 3.7e-11;
Matches 27; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

Qy 1 EACNLPVIRGPCIAFFPRMAFDVAVKGVLPFYGGCGGNGNKFYSEKRECYG 54
Db 1 EVCSGQMETGPCRAMISRWYDVTGKCVFPFYGGCGGNNRNFPTBEXCMAYC 54

RESULT 16

A32282

A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A>Note: alternative splice form APP(695)
R.lemaitre, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:G871360
A>Note: alternative splice form APP(695)
R. la Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A>Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDN:AAI3654.1; PID:G516074
R. Johnstone, E.M.; Chaney, M.O.; Moore, R.B.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JON>
A:Cross-references: GB:M29270; NID:G178863; PIDN:AA51768.1; PID:G178865
R. Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A>Note: 693-Gln was found in DNA isolated from HCHMA-D patients
R. Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A>Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39452
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:G178613; PIDN:AA59502.1; PID:G178616
A:Accession: I39451
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A:Molecule type: DNA
A:Residues: 1-530 'OMLMPVLPAPFWEAKVGR' <YOS2>
A:Cross-references: GB:M34875; NID:G178608; PIDN:AA59501.1; PID:G178615
R. Yoshikaki, S.I.; Sasaki, H.; Don-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Accession: A59020
A:Contents: annotation; extract
A>Note: revised physical map for reference I39451
R. Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A>Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:G178618; PIDN:AA51727.1; PID:G178620
A>Note: a mutation with 693-Gln is presented
R. Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A>Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:G236720; PIDN:AA19991.1; PID:G236721
R. Kamino, K.; Orr, H.T.; Payami, H.; Wiseman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
ataki, S.E.; Korenberg, J.R.; Shatma, V.; Kukul, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:G257377; PIDN:AA23645.1; PID:G257378
A:Experimental source: familial Alzheimer disease family 17
A>Note: sequence extracted from NCBI backbone (NCBI:P115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:G257379; PIDN:AA23646.1; PID:G257380
A:Experimental source: familial Alzheimer disease family 17
A>Note: sequence extracted from NCBI backbone (NCBI:P115376)
A>Note: this sequence has a silent mutation
R. Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:G28526
A>Note: alternative splice form APP(695)
R. Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:G178539; PIDN:AA51722.1; PID:G178540
A>Note: the authors translated the codon GAG for residue 647 as Asp
R. Goldberg, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:G178706; PIDN:AA35540.1; PID:G178707
A:Experimental source: brain
R. Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15533; NID:G177957; PIDN:AA51564.1; PID:G177958
R. Dykes, T.; Weidmann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DVR>
R. Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID:G289612
A:Experimental source: promyelocytic leukemia cell line HL60
A>Note: alternative splice form APP(751)

R.Ponte, P.; Gonzalez-DeWitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Notes: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <RT>
A:Cross-references: GB:X06991; NID:g28816; PIDN:CAA30041.1; PID:g292611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form SAV(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid CDNA's cloned from the brains of three F
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zahn, S.B.; Salin, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid CDNA derived from mRNA of the Alzheimer disease by
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M8734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as GLY, ACC for residue 603
8 as VAL, GGG for residue 609 as ASP, AAT for residue 610 as GLY, and GGT for residue 65
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Macera, C.L.; Multaup, G.; Stimm, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 44.4%; Score 146; DB 1; Length 770;
Best Local Similarity 48.1%; Pred. No. 9, 3e-10;
Matches 26; Conservative 4; Mismatches 24; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGNKFYSEKRECYC 54
Db 289 EVCSEQAEATGCPKRAMISRWYFDVTEGKCAFPFYGGCGGNRNPFTEYCMACVCG 342

RESULT 22
T26063
hypothetical protein W01F3.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26063
R:Cummings, P.
Submitted to the EMBL Data Library, March 1997
A:Reference number: Z20145
A:Accession: T26063
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-2225 <WIL>
A:Cross-references: UNIPROT:Q45881; EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W0
A:Experimental source: clone W01F3
C:Genetics:

A:Gene: CESP:W01F3.3
A:Map position: 5
A:introns: 33/1, 56/1, 100/1, 142/3, 271/3, 451/1, 525/3, 774/1, 1093/1, 1178/1, 1221/1;
Query Match 44.4%; Score 146; DB 2; Length 2225;
Best Local Similarity 47.2%; Pred. No. 2, 5e-09;
Matches 25; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGNKFYSEKRECYC 53
Db 1121 ECKLPVEGPGCKAFADRWYVDDGTCHPFRYGGCGGNRNHFFYQKEGVHC 1173

RESULT 23
T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23573
R:McMurray, A.
Submitted to the EMBL Data Library, June 1996
A:Reference number: Z19762
A:Accession: T23573
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-922 <WIL>
A:Cross-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA99886.1; GSPDB:GN00019; CESP:K1
A:Experimental source: clone K10D3
C:Genetics:
A:Gene: CESP:K10D3.4
A:Map position: 1
A:introns: 60/1, 228/1, 278/1, 355/1, 743/1, 802/1, 885/2

Query Match 43.8%; Score 144; DB 2; Length 922;
Best Local Similarity 49.0%; Pred. No. 1, 9e-09;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 3 CNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGNKFYSEKRECYC 53
Db 411 CKLPREGNGCTGYSNRWFMNKTGCEFIYSGCGGNANFTYECQDYC 461

RESULT 24
S30332
proteinase inhibitor (Kunitz-type) - sea anemone (Stichodactyla helianthus)
C:Species: Stichodactyla helianthus, Stichodactis helianthus (Caribbean sea anemone)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S30332
R:Antuch, W.; Berndt, K.D.; Chavez, M.A.; Delfin, J.; Wuehrlich, K.
Eur. J. Biochem. 212, 675-684, 1993
A:Title: The NMR solution structure of a Kunitz-type proteinase inhibitor from the sea a
A:Reference number: S30332; MUID:93215644; PMID:8462542
A:Accession: S30332
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-55 <ANT>
A:Cross-references: UNIPROT:P31713
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 42.6%; Score 140; DB 2; Length 55;
Best Local Similarity 49.0%; Pred. No. 4, 5e-10;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 3 CNLPYRGPCIAFPFPMADAVKGCVLFPYGGCGGNGNKFYSEKRECYC 53
Db 3 CSEPKYGRCKGYPRFYDSEGTGCTPFYVGGCGGNGNFFETLHQCRALC 53

RESULT 25
T1VITI
venom basic proteinase inhibitor I - western sand viper
N:Alternate names: venom trypsin inhibitor I

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:11:56 ; Search time 389 Seconds

(without alignments)
852.159 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPIVRGPCIAPFPRWA.....j.....QGNKMFYSEKREYCVGP 56

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390296 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2.1/USPTO/US10038722/runat.18022005.145235.14309/app_query.fasta.1.199
-DB=N Geneseq.16Dec04 -QFMT=fastap -SUFFIX=ing -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25
-MODE=LOCAL -OUTFMT=ptc -NOR=ext -HARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10038722@cgn.1.1.644@runat.18022005.145235.14309 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq.16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	190	10	ADP42040 Albumin f
2	329	100.0	190	13	ADP90032 C-termina
3	329	100.0	195	10	ADP42039 Albumin f
4	329	100.0	195	13	ADP90031 N-termina
5	329	100.0	207	10	ADP42055 DX-890 DN

6	329	100.0	207	13	ADP90047
7	329	100.0	429	10	ACF04571
8	329	100.0	444	2	AAT35167
9	329	100.0	445	10	ACF04569
10	329	100.0	1965	10	ADP42043
11	329	100.0	1965	10	ADP42041
12	329	100.0	1965	13	ADP90035
13	329	100.0	1965	13	ADP90033
14	329	100.0	3255	10	ADP42053
15	329	100.0	3255	13	ADP90045
16	329	100.0	3440	13	ADP90048
17	329	100.0	3441	10	ADP42056
18	329	100.0	3444	10	ADP42068
19	329	100.0	3444	13	ADP90019
20	324	98.5	8584	2	AAT35166
21	324	98.5	8590	2	AAT35168
22	296	90.0	204	2	AAT79078
23	296	90.0	204	2	AAV40045
24	296	90.0	210	2	AAQ78607
25	296	90.0	210	2	AAQ64758
26	296	90.0	210	2	AAQ64756
27	296	90.0	295	2	AAQ24151
28	296	90.0	307	2	AAQ41875
29	296	90.0	313	2	AAQ24143
30	296	90.0	313	2	AAQ41870
31	296	90.0	339	2	AAQ06879
32	296	90.0	344	2	AAQ54328
33	296	90.0	372	2	AAT79080
34	296	90.0	372	2	AAT79081
35	296	90.0	380	2	AAQ78612
36	296	90.0	408	9	ACH21498
37	296	90.0	435	2	AAT79083
38	296	90.0	441	2	AAV40046
39	296	90.0	467	2	AAT79086
40	296	90.0	467	2	AAT79088
41	296	90.0	540	2	AAT79087
42	296	90.0	635	2	AAT75154
43	296	90.0	666	2	AAT75155
44	296	90.0	1123	6	ABK55655
45	296	90.0	1232	1	AAH81432

ALIGNMENTS

RESULT.1	ADP42040 standard; cDNA, 190 BP.
ID	ADP42040
XX	XX
AC	ADP42040;
XX	XX
DT	12-FEB-2004 (first entry)
XX	XX
DE	Albumin fusion protein-related C-terminal BamHI-HindIII DX-890 cDNA.
XX	XX
KW	albumin fusion; Kunitz domain; cytosolic; haemostatic;
KW	hereditary angioedema; cancer; bleeding; gene therapy; DX-890; ss.
OS	Unidentified.
XX	XX
PN	WO2003066824-A2.
XX	XX
PD	14-AUG-2003.
XX	XX
PF	07-FEB-2003; 2003WO-US003616.
XX	XX
PR	07-FEB-2002; 2002US-0355547P.
XX	XX
PA	(AVET) AVENTIS BEHRING GMBH.
PA	(AVET) AVENTIS BEHRING LLC.
PA	(DELTA) DELTA BIOTECHNOLOGY LTD.
XX	(DYAX-) DYAX CORP.
PI	Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;

PI Ley AC;
XX
XX WPI; 2003-731497/69.
XX
XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
XX Example 23; Page 73; 110pp; English.
XX
XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cystostatic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related C-terminal BamHI-
CC HindIII DX-890 cDNA of the invention.
XX
SQ Sequence 190 BP; 46 A; 30 C; 51 G; 63 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,1e-36 Length: 190
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-038-722-27 (1-56) x ADF42040 (1-190)
QY 1 GIUALACysAenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 13 GAAGCTGTAACCTTGCATTTGTAGAGTCCATGATGCTTTCTTCCCAAGATGGGCT 72
QY 21 PheAspAlaValIleGlyGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 73 TTCGATGCTGTTAAGGTAAGTGTGTTTGTCCCATATGAGTGTGTCAAGTAAAGCT 132
QY 41 AsnLysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56
DB 133 AACCAAGTCTACTCTGAAAAAGAAATGATAGAAATACTGTGTTCCA 180
RESULT 2
ADP90032
ID ADR90032 standard; cDNA; 190 BP.
XX
XX ADR90032;
XX
XX 18-NOV-2004 (first entry)
XX
XX C-terminal BamHI-HindIII DX-890 cDNA.
XX
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;
XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
XX cytosstatic; haemostatic; DX-890; ss.
XX
XX Unidentified.
XX
XX US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX (LADN/) LADNER R. C.
XX (LEVA/) LEY A C.
XX
XX Ladhner RC, Ley AC;
PI

XX
XX WPI; 2004-625120/60.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
PT
XX
XX Example 7; SEQ ID NO 57; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cystostatic and haemostatic agent. The present sequence is a C-terminal
CC BamHI-HindIII DX-890 cDNA. This sequence is used in the exemplification
CC of the invention.
XX
SQ Sequence 190 BP; 46 A; 30 C; 51 G; 63 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,1e-36 Length: 190
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-038-722-27 (1-56) x ADR90032 (1-190)
QY 1 GIUALACysAenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 13 GAAGCTGTAACCTTGCATTTGTAGAGTCCATGATGCTTTCTTCCCAAGATGGGCT 72
QY 21 PheAspAlaValIleGlyGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 73 TTCGATGCTGTTAAGGTAAGTGTGTTTGTCCCATATGAGTGTGTCAAGTAAAGCT 132
QY 41 AsnLysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56
DB 133 AACCAAGTCTACTCTGAAAAAGAAATGATAGAAATACTGTGTTCCA 180
RESULT 3
ADP42039
ID ADF42039 standard; cDNA; 195 BP.
XX
XX ADF42039;
XX
XX 12-FEB-2004 (first entry)
XX
XX Albumin fusion protein-related N-terminal BgIII-BamHI DX-890 cDNA.
XX
XX albumin fusion; Kunitz domain; cytosstatic; haemostatic;
XX hereditary angioedema; cancer; bleeding; gene therapy; DX-890; ss.
XX
XX Unidentified.
XX
XX WO2003066824-A2.
XX
XX 14-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003616.
XX
XX 07-FEB-2002; 2002US-0355547P.
XX
XX (AVET) AVENTIS BEHRING GMBH.
XX (AVET) AVENTIS BEHRING LLC.
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX (DVAX-) DVAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladhner RC;
XX Ley AC;
PI

DR WPI; 2003-731497/69.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.

XX Example 23; Page 73; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytosolic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related N-terminal BgIII-
CC BamHI DX-890 CDNA of the invention.

XX Sequence 195 BP; 49 A; 30 C; 53 G; 63 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1,14e-36	Length:	195
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-038-722-27 (1-56) x ADF42039 (1-195)

QY 1 GluAlaCyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 19 GAAGCTGTAACTTCCCAATTGTTAGAGTCCATGTATGCTTTCTTCCCAAGATGGCT 78

QY 21 PheAspAlaValLysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 79 TTCATGCTGTAAAGGTAAGTGTGTTTGTCCATATGTTGTTGTCACAGGTAAACGCT 138

QY 41 AsnLysPheTyrSerGlyLysGlyCysArgGlyLysTyrCysGlyValPro 56
DB 139 AACCAAGTCTACTCTGAAGAAAGATGTAGAGATGACTGGTGTCCA 186

RESULT 4

ADP42031

ID ADR90031 standard; cDNA; 195 BP.

AC ADR90031;

DT 18-NOV-2004 (first entry)

DE N-terminal BgIII-BamHI DX-890 CDNA.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytosolic; haemostatic; DX-890; ss.

XX Undifferentiated.

OS US2004171794-A1.

PN 02-SEP-2004.

PD 07-FEB-2003; 2003US-00361997.

PR 07-FEB-2003; 2003US-00361997.

PA (LADN/) LADNER R C.
PA (LEYA/) LEY A C.
PI Ladner RC, Ley AC;
DR WPI; 2004-625120/60.

XX New Kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
PT Example 7; SEQ ID NO 56; 123pp; English.

XX The invention relates to proteins comprising Kunitz domain peptide,
CC designated DPT-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytosolic and haemostatic agent. The present sequence is a N-terminal
CC BgIII-BamHI DX-890 CDNA. This sequence is used in the exemplification of
CC the invention.

XX Sequence 195 BP; 49 A; 30 C; 53 G; 63 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1,14e-36	Length:	195
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-038-722-27 (1-56) x ADR90031 (1-195)

QY 1 GluAlaCyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 19 GAAGCTGTAACTTCCCAATTGTTAGAGTCCATGTATGCTTTCTTCCCAAGATGGCT 78

QY 21 PheAspAlaValLysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 79 TTCATGCTGTAAAGGTAAGTGTGTTTGTCCATATGTTGTTGTCACAGGTAAACGCT 138

QY 41 AsnLysPheTyrSerGlyLysGlyCysArgGlyLysTyrCysGlyValPro 56
DB 139 AACCAAGTCTACTCTGAAGAAAGATGTAGAGATGACTGGTGTCCA 186

RESULT 5

ADP42055

ID ADF42055 standard; DNA; 207 BP.

AC ADF42055;

DT 12-FEB-2004 (first entry)

DE DX-890 DNA which was inserted at BspEI/XpnI site of pDB2300X2.

XX albumin fusion; Kunitz domain; cytosolic; haemostatic;
KW hereditary angioedema; cancer; bleeding; gene therapy;
KW plasmid pDB2300X2 NotI expression cassette; ds; DX-890.

XX Undifferentiated.

OS WO2003066824-A2.

PN 14-AUG-2003.

PD 07-FEB-2003; 2003WO-US003616.

PR 07-FEB-2002; 2002US-0355547P.

PA (AVET) AVENTIS BEHRING GMBH.
PA (AVET) AVENTIS BEHRING LLC.
PA (DEL2) DELTA BIOTECHNOLOGY LTD.
PA (DYAX-) DYAX CORP.
PI Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;
DR WPI; 2003-731497/69.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
 PT useful for preparing a composition for treating a patient with hereditary
 PT angiodema or angiodema-related disease, cancer or bleeding disorder.

XX Example 23; Page 89; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a
 CC Kunitz domain peptide or its fragment or variant and an albumin or its
 CC fragment or variant. The fusion protein of the invention demonstrates
 CC cytosolic and haemostatic activities and may be useful for preparing a
 CC composition for treating a patient with hereditary angiodema, an
 CC angiodema-related disease, cancer, a cancer-related disease or a
 CC bleeding disorder, as well as during gene therapy procedures. The current
 CC sequence is that of the DX-890 DNA of the invention which was inserted at
 CC BspRI/KpnI site of plasmid pDB2300X2 modified NotI expression cassette.

XX SQ Sequence 207 BP; 37 A; 51 C; 59 G; 60 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,23e-36	Length:	207
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-038-722-27 (1-56) x ADR42055 (1-207)

QY 1 GIUAIAQYASnleuProIleValAArgLYProCYsileAlaPhePheProArgTPala 20
 DB 28 GAGGCTTGCAATCTTCCTATGCTCCGCGCCCTTGCAATGCTTTTCTCTGCGGCC 87
 QY 21 PheAPalaValIyGlyLYsCYsValleuPheProTYrGlyGlyCYsGInGlyAsnGly 40
 DB 88 TTGACGCGCGCAAGCAAAAGCGCTCTTTCTTCTTACGCGGCTTGCAGGCGCATGCG 147
 QY 41 AsnLYsPheTYrSerGlyLYsGlyCYsAArgLYrCYsGlyValPro 56
 DB 148 AATAAATTATTATAGCGAAGAGAGTCCCTGATGATGGCGCTCCT 195

RESULT 6

ADR90047
 ID ADR90047 standard; cDNA; 207 BP.

XX ADR90047;

XX 18-NOV-2004 (first entry)

XX DX-890 coding region cDNA.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
 KW hereditary angiodema; cancer; chronic obstructive pulmonary disease;
 KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
 KW cytosolic; haemostatic; DX-890; ss.

XX Unidentified.

XX US2004171794-A1.

XX 02-SEP-2004.

XX 07-FEB-2003; 2003US-00361997.

XX 07-FEB-2003; 2003US-00361997.

XX (LADN/) LADNER R C.

XX (LEYA/) LEY A C.

XX LADNER RC, LEY AC;

XX WPI; 2004-625120/60.

PT New kunitz domain peptide useful as human neutrophil elastase inhibitor
 PT for the treatment of e.g. cystic fibrosis and related disease.

XX Example 19; SEQ ID NO 72; 123pp; English.

XX The invention relates to proteins comprising kunitz domain peptide,
 CC designated Dpi-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angiodema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cytosolic and haemostatic agent. The present sequence is a DX-890 coding
 CC region cDNA. This sequence is used in the exemplification of the
 CC invention.

XX SQ Sequence 207 BP; 37 A; 51 C; 59 G; 60 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,23e-36	Length:	207
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-038-722-27 (1-56) x ADR90047 (1-207)

QY 1 GIUAIAQYASnleuProIleValAArgLYProCYsileAlaPhePheProArgTPala 20
 DB 28 GAGGCTTGCAATCTTCCTATGCTCCGCGCCCTTGCAATGCTTTTCTCTGCGGCC 87
 QY 21 PheAPalaValIyGlyLYsCYsValleuPheProTYrGlyGlyCYsGInGlyAsnGly 40
 DB 88 TTGACGCGCGCAAGCAAAAGCGCTCTTTCTTCTTACGCGGCTTGCAGGCGCATGCG 147
 QY 41 AsnLYsPheTYrSerGlyLYsGlyCYsAArgLYrCYsGlyValPro 56
 DB 148 AATAAATTATTATAGCGAAGAGAGTCCCTGATGATGGCGCTCCT 195

RESULT 7

ACF04571
 ID ACF04571 standard; DNA; 429 BP.

XX ACF04571;

XX 04-DEC-2003 (first entry)

XX Fusion sequence of alpha mating factor and EPI-hNE-4 coding sequences.

XX EPI-hNE-4; EPI-hNE; alpha mating factor prepropeptide; fusion gene; gene;
 KW mutagenic; ds.

XX Saccharomyces cerevisiae.

XX Pichia pastoris.

XX WO2003062431-A2.

XX 31-JUL-2003.

XX 23-JAN-2003; 2003WO-EP001212.

XX 23-JAN-2002; 2002EP-00290166.

XX (DEBI-) DEBIOPHAM SA.

XX Gerard C, Poncin A, Saudubray F, Petchot-Bacque J;

XX WPI; 2003-598755/56.

XX P-PSDB; ABR84585.

XX New fused gene constructs and expression vectors, useful for transforming
 PT microorganisms (particularly the yeast Pichia pastoris) for use in
 PT producing e.g. EPI-hNE-4 proteins with very low levels of its improperly

PF processed form.
XX
XX
PS Claim 3; Fig 9; 27pp; English.
XX
CC The present invention relates to a fused gene construct, which comprises
CC a nucleotide sequence coding for the Saccharomyces cerevisiae alpha
CC mating factor prepeptide or its variant, which is modified so as to
CC replace the lysine residue in position 76 of the amino acid sequence of
CC the naturally occurring prepeptide by an Alanine residue. The
CC nucleotide sequence is ligated to the 5' terminal of a nucleotide
CC sequence coding for EPI-hNE-4. An expression vector for the sequence is
CC also claimed. The gene construct or vector is useful for transforming
CC microorganisms (particularly yeast) to produce EPI-hNE-4 protein with
CC very low levels of its improperly processed form. The gene construct,
CC nucleotide sequence, expression vector or microorganism is useful for
CC producing or secreting a protein, particularly EPI-hNE-4, which contains
CC undetectable levels of the EPI-hNE-4 (n+9). This facilitates further
CC purification steps, and therefore results in economies both on the
CC financial and time-spent scale. The present sequence is a fusion sequence
CC containing the S. cerevisiae alpha mating factor prepeptide coding
CC sequence and the Pichia pastoris EPI-hNE-4 coding sequence and used in
CC the exemplification of the invention
XX
SQ Sequence 429 BP; 91 A; 100 C; 102 G; 136 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,19e-36 Length: 429
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-038-722-27 (1-56) x ACF04571 (1-429)

QY 1 GluAlaCySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAla 20
Db 256 GAGGCTGTAACTTCCCAATCGTCAGAGGTCATGCTTCTTCCCAAGATGGGCT 315

QY 21 PheAspAlaValIlySGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnIly 40
Db 316 TTCGACGCTTTAAAGGTAAGTGCCTGTTCCCATACGGGTGTGTCAGAGTAACGCT 375

QY 41 AsnIlyPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56
Db 376 AACCAAGTTCTACTCTGAGAAAGAGTGTAGAGAGTCTGTGTTCCTCA 423

RESULT 8
AAT35167
ID AAT35167 standard; DNA; 444 BP.
XX
AC AAT35167;
XX
DT 14-FEB-1997 (first entry)
XX
DE EPI-HNE-4 Modified Kunitz domain expression cassette.
XX
KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 10..435
FT /tag= a
FT /product= "EPI-HNE-4 modified Kunitz domain"
XX
XX MO9620278-A2.
XX
XX 04-JUL-1996.

PF 15-DEC-1995; 95WO-US016349.
XX
XX
PR 16-DEC-1994; 94US-00358160.
XX
XX
PA (PROT-) PROTEIN ENG CORP.
XX
PI Ley AC, Lather RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX
DR WPI; 1996-321851/32.
DR P-PEDB; AAR99215.
XX
XX
PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
PS Example 10; Page 75; 105pp; English.
XX
XX Genetically engineered human derived Kunitz domains can be used to
XX inhibit human neutrophil elastase, an enzyme involved in the elimination
XX of pathogens and the restructuring of connective tissue. In cases of
XX reduction of the circulating alpha-1-protease inhibitor (API or alpha
XX antitrypsin), or the inactivation of API by oxidation (smokers
XX emphysema), extensive destruction of the lung tissue may result from
XX uncontrolled elastolytic activity of human neutrophil elastase. Other
XX respiratory disorders such as cystic fibrosis are thought to be caused by
XX human neutrophil elastase release by neutrophils. The genetically
XX engineered human derived Kunitz domains can be used to treat such
XX respiratory disorders. See AAR99146-R99211. Fusion genes were used in the
XX production of the Kunitz domain derivatives. Protein expression cassettes
XX are then cloned into the plasmid pHI-D2 using BamBI and EcoRI
XX restriction sites. The cloned sequence is under the transcriptional
XX control of Pichia pastoris axi gene promoter and regulatory sequences
XX and downstream polyadenylation and transcription termination sequences.
XX Transformed strains of P. pastoris were used to express the various EPI-
XX hNE proteins derived from the EPI and ITI-D2 Kunitz domains. This
XX sequence is a BamBI-AccII-EcoRI expression cassette for expression of EPI-
XX hNE-4
SQ Sequence 444 BP; 98 A; 102 C; 105 G; 139 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,34e-36 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-038-722-27 (1-56) x AAT35167 (1-444)

QY 1 GluAlaCySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrAla 20
Db 265 GAGGCTGTAACTTCCCAATCGTCAGAGTTCATGCTTCTTCCCAAGATGGGCT 324

QY 21 PheAspAlaValIlySGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnIly 40
Db 325 TTCGACGCTTTAAAGGTAAGTGCCTGTTCCCATACGGGTGTGTCAGAGTAACGCT 384

QY 41 AsnIlyPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56
Db 385 AACCAAGTTCTACTCTGAGAAAGAGTGTAGAGAGTCTGTGTTCCTCA 432

RESULT 9
ACF04569
ID ACF04569 standard; DNA; 445 BP.
XX
AC ACF04569;
XX
XX
DT 04-DEC-2003 (first entry)
XX
XX P. pastoris prepro-EPI-hNE-4 mutated coding sequence.
XX
XX EPI-hNE-4; EPI-hNE; alpha mating factor prepeptide; gene; mutant;
XX

KW mutagenic; ds.
XX
OS Pichia pastoris.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 10..435
FT /*tag= a
FT /product= "mutated prepro-Epi-hNE-4"
XX
XX WO2003062431-A2.
XX
XX 31-JUL-2003.
XX
XX 23-JAN-2003; 2003WO-EP001212.
XX
XX 23-JAN-2002; 2002EP-00290166.
XX
XX (DEBI-) DEBIOPHARM SA.
XX
XX Gerard C, Poncin A, Saudubray F, Petchot-Bacque J;
XX
XX WPI; 2003-598755/56.
XX
XX P-PSDB; ABR84583.
XX
XX New fused gene constructs and expression vectors, useful for transforming
XX microorganisms (particularly the yeast Pichia pastoris) for use in
XX producing e.g. Epi-hNE-4 proteins with very low levels of its improperly
XX processed form.
XX
XX Example 2; Fig 1B; 27pp; English.
XX
XX The present invention relates to a fused gene construct, which comprises
XX a nucleotide sequence coding for the Saccharomyces cerevisiae alpha
XX mating factor prepropeptide or its variant, which is modified so as to
XX replace the lysine residue in position 76 of the amino acid sequence of
XX the naturally occurring prepropeptide by an Alanine residue. The
XX nucleotide sequence is ligated to the 5' terminal of a nucleotide
XX sequence coding for Epi-hNE-4. An expression vector for the sequence is
XX also claimed. The gene construct or vector is useful for transforming
XX microorganisms (particularly yeast) to produce Epi-hNE-4 protein with
XX very low levels of its improperly processed form. The gene construct,
XX nucleotide sequence, expression vector or microorganism is useful for
XX producing or secreting a protein, particularly Epi-hNE-4, which contains
XX undetectable levels of the Epi-hNE-4 (n+9). This facilitates further
XX purification steps, and therefore results in economies both on the
XX financial and time spent scale. The present sequence is a mutated version
XX of the Pichia pastoris Epi-hNE-4 coding sequence used in the
XX exemplification of the invention
XX
XX SQ Sequence 445 BP; 96 A; 104 C; 105 G; 140 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 3,34e-36 Length: 445
XX Score: 329.00 Matches: 56
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 10 Gaps: 0
XX
XX US-10-038-722-27 (1-56) x ACF04569 (1-445)
XX
XX 1 GIUUAACyAAsnLeuProIleValArgGIyProCyAIIeAlAPhePheProArGTpAla 20
XX |||||
XX 265 GAGGCTTGAACCTTCCCAATCGTCAGAGGTCATGCAATTCCTTCCCAAGATGGGCT 324
XX |||||
XX 21 PheAspAlaValIysGIyIyScyValLeuPheProTyGIyGIyCysGlnIyAsnGIy 40
XX |||||
XX 325 TTCGACGCTGTAAAGGTAAAGTCCGCTTCTTCCATAGCGGTGTCAAGGTAAACGT 384
XX |||||
XX 41 AsnIySPheTySerGIyIyScyValArgGIyIyCysGIyValPro 56
XX |||||
XX 385 AACCAAGTCTACTGTGAGGAGGTGTAGAGAGTACTGTGTGTTC 432

RESULT 10
ADP42043
ID ADP42043 standard; DNA; 1965 BP.
XX
XX AC ADP42043;
XX
XX 12-FEB-2004 (first entry)
XX
XX C-terminal albumin-(GGS)4GG-DX-890 fusion DNA.
XX
XX albumin fusion; Kunitz domain; cytostatic; haemostatic;
XX hereditary angioedema; cancer; bleeding; gene therapy;
XX C-terminal albumin-(GGS)4GG-DX-890 fusion; ds; gene.
XX
XX Synthetic.
XX Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT CDS 1..1965
XX FT /*tag= a
XX FT /partial
XX FT /product= "C-terminal albumin-(GGS)4GG-DX-890 fusion
XX FT protein
XX FT /note= "No start or stop codon"
XX
XX WO2003066824-A2.
XX
XX 14-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003616.
XX
XX 07-FEB-2002; 2002US-035547P.
XX
XX (AVET) AVENTIS BEHRING GMBH.
XX (AVET) AVENTIS BEHRING LLC.
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX (DYAX-) DYAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
XX ley AC;
XX
XX WPI; 2003-731497/69.
XX
XX P-PSDB; ADP42044.
XX
XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
XX useful for preparing a composition for treating a patient with hereditary
XX angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
XX Example 23; Page 77-76; 110pp; English.
XX
XX The invention relates to a novel albumin fusion protein comprising a
XX Kunitz domain peptide or its fragment or variant and an albumin or its
XX fragment or variant. The fusion protein of the invention demonstrates
XX cytostatic and haemostatic activities and may be useful for preparing a
XX composition for treating a patient with hereditary angioedema, an
XX angioedema-related disease, cancer, a cancer-related disease or a
XX bleeding disorder, as well as during gene therapy procedures. The current
XX sequence is that of the C-terminal albumin-(GGS)4GG-DX-890 fusion DNA of
XX the invention.
XX
XX SQ Sequence 1965 BP; 586 A; 383 C; 469 G; 527 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2,32e-35 Length: 1965
XX Score: 329.00 Matches: 56
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 10 Gaps: 0
XX
XX US-10-038-722-27 (1-56) x ADP42043 (1-1965)

Oy	1	GIuAlaCyAsnAlaLeuProCilLeValArgGlyProCysIleAlaPhePheProArgTrpAla	20
Db	1798	GAAGCTTAACTTACTCCAAATGTTAGAGGTCATGATTCCTTCTCCCAAGATGGCT	185
Oy	21	PheAspAlaValIlyeGlyLysCySeValIleuPheProTYrGlyGlyCySeGlnIyAsnGly	40
Db	1858	TTTCATGCTGTTTAAGGTTAAGTGCTTTTGTTCCTATATGGTGCTTCAAGTAAAGCT	191
Oy	41	AsnIysPheTYrSerGluIyGlyCysArgGlyIYrCySeGlyValPro	56
Db	1918	AACAAGTTCTACTCTGAAAAAGAAATGTAGAAATAGTCTGGTGTTCCA	1965
RESULT 11			
ADP42041			
ID	ADP42041	standard; DNA; 1965 BP.	
XX	ADP42041;		
XX	12-FEB-2004	(first entry)	
XX			
XX		N-terminal DX-890-(GGS)4GG-albumin fusion DNA.	
XX			
XX		albumin fusion; Kunitz domain; cytostatic; haemostatic;	
KW		hereditary angioedema; cancer; bleeding; gene therapy;	
KW		N-terminal DX-890-(GGS)4GG-albumin fusion; ds; gene.	
XX			
OS		Synthetic.	
XX		Unidentified.	
XX			
FT	Key	Location/Qualifiers	
FT	CDS	1..1965	
FT		/*tag= a	
FT		/partial	
FT		/product= "N-terminal DX-890-(GGS)4GG-albumin fusion	
FT		protein"	
FT		/note= "No start or stop codon"	
XX			
FN	WO2003066824-A2.		
PD	14-AUG-2003.		
XX			
XX	07-FEB-2003; 2003WO-US003616.		
PE			
XX	07-FEB-2002; 2002US-0355547P.		
XX			
PA	(AVET) AVENTIS BEHRING GMBH.		
PA	(AVET) AVENTIS BEHRING LLC.		
PA	(DELZ) DELTA BIOTECHNOLOGY LTD.		
PA	(DYAX-) DYAX CORP.		
XX			
PI	Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;		
PI	Ley AC;		
XX			
DR	WPI; 2003-731497/69.		
XX			
XX	P-PSDB; ADP42042.		
PT			
PT		Albumin fusion protein comprising a Kunitz domain peptide and an albumin,	
PT		useful for preparing a composition for treating a patient with hereditary	
PT		angioedema or angioedema-related disease, cancer or bleeding disorder.	
XX			
XX			
PS	Example 23; Page 74; 110pp; English.		
XX			
XX			
CC		The invention relates to a novel albumin fusion protein comprising a	
CC		Kunitz domain peptide or its fragment or variant and an albumin or its	
CC		fragment or variant. The fusion protein of the invention demonstrates	
CC		cytostatic and haemostatic activities and may be useful for preparing a	
CC		composition for treating a patient with hereditary angioedema, an	
CC		angioedema-related disease, cancer, a cancer-related disease or a	
CC		bleeding disorder, as well as during gene therapy procedures. The current	
CC		sequence is that of the N-terminal DX-890-(GGS)4GG-albumin fusion DNA of	
CC		the invention.	
XX			
XX			
SO	Sequence 1965 BP; 540 A; 386 C; 477 G; 562 T; 0 U; 0 Other;		

Alignment Scores:	2,32e-35	Length:	1965
Pred. No.:		Matches:	56
Score:	329.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	10		

US-10-038-722-27 (1-56) x ADR#42041 (1-1965)	
QY	1 GUAlAlCYsAsnIuProlIeValaRgSlProCYsIllealaphPheProArGTpAla 20
DB	1 GAAGCTGTAACTGGCAATGTGTAGAGTCCATGTATGCTTCTTCCCAAGATGAGCT 60
QY	21 PhAsPAlaValIyEGlYyCyEysValIuPheProTYRgIyGyCGlNGIyAsnGIy 40
DB	61 TTGGAAGCTGTAAAGGTAAAGTGTATTTGTTCCATVGGTGTGTCAAGGTAAAGCT 120
QY	41 AsnIyPheTYSerGIuPysIuCYsArRgIuTYRyCYsGIyValPro 56
DB	121 AACAACTTCTACTCTGAAAGCAATGTAGAGAAATCTGTGTGTTCCA 168

RESULT 12	
ADR30035	
ID	ADR90035 standard; DNA; 1965 BP.
XX	
AC	ADR90035;
XX	
DT	18-NOV-2004 (first entry)
DE	C-terminal DX-890- (GGS) 4 GG-albumin fusion DNA.
XX	
KW	Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW	hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW	asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW	cytostatic; haemostatic; chimeric; DX-890; human albumin; HA; human;
KW	gene; ds.
OS	Homo sapiens.
OS	Chimeric.
OS	Unidentified.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1965
FT	/*tag= a
FT	/product= "C-terminal DX-890- (GGS) 4 GG-albumin fusion
FT	protein
FT	/partial
FT	/note= "No start and stop codon"
XX	
PN	US2004171794-A1.
XX	
PD	02-SEP-2004.
XX	
PF	07-FEB-2003; 2003US-00361997.
XX	
PR	07-FEB-2003; 2003US-00361997.
XX	
PA	(LADN/) LADNER R C.
XX	
PA	(LEYA/) LEY A C.
XX	
P1	Ladner RC, Ley AC;
XX	
WP1	WP1; 2004-625120/60.
DR	P-PSDB; ADR90036.
XX	
PT	New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX	for the treatment of e.g. cystic fibrosis and related disease.
PS	Example 9; SEQ ID NO 60; 123pp; English.
XX	
CC	The invention relates to proteins comprising kunitz domain peptide,

CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cystostatic and haemostatic agent. The present sequence is a C-terminal DX
CC -890-(GGS)4 GG-albumin fusion DNA. This fusion DNA contains DX-890 cDNA,
CC GS linker region and human albumin (HA). This sequence is used in the
CC exemplification of the invention.

XX SQ Sequence 1965 BP; 586 A; 383 C; 469 G; 527 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,32e-35	Length:	1965
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-038-722-27 (1-56) x ADR90035 (1-1965)

QY 1 GIuAlaCyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrPa 20

Db 1798 GAAGCCTGTAACCTGCCAATGTTAGAGGTCATGATGCTTCTCCCAAGATGGGCT 1857

QY 21 PheAepAlaValIyGlyLysCySeValLeuPheProTyrGlyGlyCysGlnGlyAangly 40

Db 1858 TTCGATGCTGTAAAGGTAAAGTGTGTTGTTCCTCATATGAGTGTGAAGGTAAAGGT 1917

QY 41 AsnLysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

Db 1918 AACAGTTCTACTCTGAAAAGAAATGTAAGAATCTGTGGTGTCCA 1965

RESULT 13

ADR90033 standard; DNA; 1965 BP.

ID ADR90033

XX ADR90033;

XX 18-NOV-2004 (first entry)

XX N-terminal DX-890-(GGS)4 GG-albumin fusion DNA.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;

KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

KW cystostatic; haemostatic; chimeric; DX-890; human albumin; HA; human;

XX gene; ds.

XX Homo sapiens.

OS Chimeric.

OS Undifferentiated.

XX Key

XX US2004171794-A1.

XX 02-SEP-2004.

XX 07-FEB-2003; 2003US-00361997.

XX 07-FEB-2003; 2003US-00361997.

XX (LADN/) LADNER R C.

XX (LEVA/) LEY A C.

PI Ladder RC, Ley AC;

XX WPI: 2004-625120/60.

DR P-P8DB; ADR90034.

XX New kunitz domain peptide useful as human neutrophil elastase inhibitor

PT for the treatment of e.g. cystic fibrosis and related disease.

XX Example 8; SEQ ID NO 58; 123pp; English.

CC The invention relates to proteins comprising kunitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cystostatic and haemostatic agent. The present sequence is a N-terminal DX
CC -890-(GGS)4 GG-albumin fusion DNA. This fusion DNA contains DX-890 cDNA,
CC GS linker region and human albumin (HA). This sequence is used in the
CC exemplification of the invention.

XX SQ Sequence 1965 BP; 540 A; 386 C; 477 G; 562 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,32e-35	Length:	1965
Score:	329.00	Matches:	56
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-038-722-27 (1-56) x ADR90033 (1-1965)

QY 1 GIuAlaCyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrPa 20

Db 1 GAAGCCTGTAACCTGCCAATGTTAGAGGTCATGATGCTTCTCCCAAGATGGGCT 60

QY 21 PheAepAlaValIyGlyLysCySeValLeuPheProTyrGlyGlyCysGlnGlyAangly 40

Db 61 TTCGATGCTGTAAAGGTAAAGTGTGTTGTTCCTCATATGAGTGTGAAGGTAAAGGT 120

QY 41 AsnLysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

Db 121 AACAGTTCTACTCTGAAAAGAAATGTAAGAATCTGTGGTGTCCA 168

RESULT 14

ADP42053 standard; DNA; 3255 BP.

ID ADP42053

XX ADP42053;

XX 12-FEB-2004 (first entry)

XX Plasmid PDB2300X2 NotI modified expression cassette DNA.

KW albumin fusion; Kunitz domain; cytosstatic; haemostatic;

KW hereditary angioedema; cancer; bleeding; gene therapy;

KW plasmid PDB2300X2 NotI expression cassette; ds; gene; DX-890.

XX Synthetic.

OS Undifferentiated.

XX Key

XX MO2003066824-A2.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003616.

XX (LADN/) LADNER R C.

XX (LEVA/) LEY A C.

XX 07-FEB-2002; 2002US-0355547P.
PR
XX (AVET) AVENTIS BEHRING GMBH.
PA (AVET) AVENTIS BEHRING LLC.
PA (DEL2) DELTA BIOTECHNOLOGY LTD.
PA (DYAX-) DYAX CORP.
XX
PI Hauser H, Welmer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;
XX
DR WPI; 2003-731497/69.
DR P-PSDB; ADF42054.
XX
PT Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angiodema or angiodema-related disease, cancer or bleeding disorder.
XX
PS Example 23; Page 85-89; 110pp; English.
XX
CC The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytosolic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angiodema, an
CC angiodema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related plasmid PDB2300X2
CC modified NotI expression cassette DNA of the invention which has N-
CC terminal DX-890 and C-terminal linker ready for a second DX-890 sequence.
XX
SQ Sequence 3255 BP; 931 A; 666 C; 769 G; 889 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4,48e-35 Length: 3255
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADF42053 (1-3255)
OY 1 GIUAACysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 901 GAAGCCTGTAAGCTTGCATTTGAGAGTCCATGATGCTTTCTCCCAAGATGGCT 960
OY 21 PheAspAlaValIleGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 961 TTCGATGCTGTTAAGGTAAGTGTGTTTGTCCCATATGAGTGTGTCAGATAACGCT 1020
OY 41 AsnLysPheTyrSerGluLysGluCysArgGlyTyrCysGlnValPro 56
DB 1021 AACAGTCTACTCTGAAAGAAAGATGAGAAATCTGTGTTGCCA 1068
XX
RESULT 15
ADR90045
ID ADR90045 standard; DNA; 3255 BP.
XX
AC ADR90045;
XX
DT 18-NOV-2004 (first entry)
XX
DE PDB2300X2-2xGS linker fusion DNA.
XX
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX hereditary angiodema; cancer; chronic obstructive pulmonary disease;
XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
XX cystostatic; haemostatic; chimeric; human; rRNA synthase gene;
XX human albumin; HA; gene; ds.
XX
XX Homo sapiens.
OS
OS Chimeric.

OS Unidentified.
XX
XX Key Location/Qualifiers
FH CDS 829..2916
FT
FT
FT /tag= b
FT /product= "PDB2300X2-2xGS linker fusion protein"
FT /note= "CDS contains two stop codons"
FT 829..900
FT /tag= a
FT 901..2910
FT /tag= d
FT /product= "Mature PDB2300X2-2xGS linker fusion protein"
FT 901..1068
FT /tag= c
FT /note= "DX-890 DNA"
FT 1069..1110
FT /tag= e
FT /note= "GS-linker region DNA"
FT 1111..12865
FT /tag= f
FT /note= "rHA gene"
XX
XX US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX (LADN/) LADNER R C.
XX (LEYA/) LEY A C.
XX
XX Ladner RC, Ley AC;
XX WPI; 2004-625120/60.
XX P-PSDB; ADR90046.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Example 18; SEQ ID NO 70; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
XX designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX albumin. The invention is useful for treating cystic fibrosis and related
XX diseases, hereditary angiodema, cancer and related diseases including
XX chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX cytosolic and haemostatic agent. The present sequence is a PDB2300X2-
XX 2xGS linker fusion DNA. This chimeric DNA contains DX-890 cDNA at its N-
XX terminal end, rHA synthase gene and the linkers at its C-terminal end.
XX This sequence is used in the exemplification of the invention.
XX
SQ Sequence 3255 BP; 931 A; 666 C; 769 G; 889 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4,48e-35 Length: 3255
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADR90045 (1-3255)
OY 1 GIUAACysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 901 GAAGCCTGTAAGCTTGCATTTGAGAGTCCATGATGCTTTCTCCCAAGATGGCT 960
OY 21 PheAspAlaValIleGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 961 TTCGATGCTGTTAAGGTAAGTGTGTTTGTCCCATATGAGTGTGTCAGATAACGCT 1020

OY 41 AsnlySpheTYrSerGIuTySGluCySaRgGIuTYrCySGIyValPro 56
 DB 1021 AACAGTCTACTCTGAAAGAAATGTAGAGAAATCTGTGCTTCCA 1068
 RESULT 16
 ID ADR90048
 XX ADR90048 standard; DNA; 3440 BP.
 AC ADR90048;
 XX 18-NOV-2004 (first entry)
 DT PDB2300X3-2XDX-890 fusion DNA.
 DE Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
 XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;
 KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
 KW cystostatic; haemostatic; chimeric; human; rHA synthase gene;
 KM human albumin; HA; DX-890; gene; ds.
 XX Homo sapiens.
 OS Chimeric.
 OS Unidentified.
 XX Key
 FH 829..3090 Location/Qualifiers
 FT CDS /tag= b
 FT /product= "PDB2300X3-2XDX-890 fusion protein"
 FT /note= "CDS contains two stop codons"
 FT sig_peptide 829..900
 FT /tag= a
 FT mat_peptide 901..3084
 FT /tag= d
 FT /product= "ature PDB2300X2-2XGS linker fusion protein"
 FT misc_feature 901..1068
 FT /tag= c
 FT /note= "DX-890 DNA #1"
 FT misc_feature 1069..1110
 FT /tag= e
 FT /note= "GS-linker region DNA"
 FT misc_feature 1111..2865
 FT /tag= f
 FT /note= "rHA gene"
 FT misc_feature 2866..2901
 FT /tag= g
 FT /note= "GS-linker region DNA"
 FT misc_feature 2902..3084
 FT /tag= h
 FT /note= "DX-890 DNA #2"
 XX US2004171794-A1.
 XX 02-SEP-2004.
 PD 07-FEB-2003; 2003US-00361997.
 PF 07-FEB-2003; 2003US-00361997.
 XX 07-FEB-2003; 2003US-00361997.
 XX (LADN/) LADNER R C.
 PA (LEYA/) LEY A C.
 XX LADNER RC, LEY AC;
 XX WPI; 2004-625120/60.
 DR P-PSDB; ADR90049, ADR90050.
 XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
 PT for the treatment of e.g. cystic fibrosis and related disease.
 XX Example 19; SEQ ID NO 73; 123pp; English.
 PS The invention relates to proteins comprising kunitz domain peptide,
 CC

CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angioedema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cystostatic and haemostatic agent. The present sequence is a PDB2300X3-
 CC 2XDX-890 fusion DNA. This chimeric DNA contains two DX-890 CDNA's, rHA
 CC synthase gene and the linkers. This sequence is used in the
 CC exemplification of the invention.
 XX SQ Sequence 3440 BP; 966 A; 711 C; 820 G; 943 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4,81e-35 Length: 3440
 Score: 329.00 Matches: 56
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0
 US-10-038-722-27 (1-56) x ADR90048 (1-3440)
 OY 1 GIUAlaCYaenleuProIleValaRgGIyProCYsIleAlaPhePheProArGTrpAla 20
 DB 901 GAAGCCTGTACTCTGCAATGTGTAGAGTCCATGTGCTTCTTCCAGATGGCT 960
 OY 21 PheAepAlaValLySGIyLyCySaValLeuPheProTYrGIyGIyCySGIngIyAsnGIy 40
 DB 961 TTCATGCTGTTAAGGTGAAGTGTGTTTGTTCATATGTTGTGTGTCAGATACGCT 1020
 OY 41 AsnlySpheTYrSerGIuTySGluCySaRgGIuTYrCySGIyValPro 56
 DB 1021 AACAGTCTACTCTGAAAGAAATGTAGAGAAATCTGTGCTTCCA 1068
 RESULT 17
 ADF42056
 ID ADF42056 standard; DNA; 3441 BP.
 XX ADF42056;
 AC ADF42056;
 XX 12-FEB-2004 (first entry)
 DT Plasmid PDB2300X3 NctI modified expression cassette DNA - 2X DX-890.
 XX albumin fusion; Kunitz domain; cyostatic; haemostatic;
 KW hereditary angioedema; cancer; bleeding; gene therapy;
 KW plasmid PDB2300X3 NctI expression cassette; ds; gene; DX-890.
 XX Synthetic.
 OS Unidentified.
 OS Unidentified.
 FH Key
 FT CDS Location/Qualifiers
 FT /tag= a
 FT /product= "Plasmid PDB2300X3 NctI modified expression
 cassette protein - 2X DX-890"
 XX MO2003066824-A2.
 XX 14-AUG-2003.
 PD 07-FEB-2003; 2003WO-US003616.
 PF 07-FEB-2002; 2002US-0355547P.
 XX 07-FEB-2002; 2002US-0355547P.
 PR (AVENT) AVENTIS BEHRING GMBH.
 XX (AVENT) AVENTIS BEHRING LLC.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (DVAX-) DVAX CORP.
 XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
 PI Ley AC;
 XX

DR WPI: 2003-731497/69.
DR P-PSDB; ADF42057.
XX
PT Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
PS Example 23; Page 90-94; 110pp; English.
XX
CC The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytosolic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related plasmid PDB2300X3
CC modified NotI expression cassette DNA of the invention which has 2 DX-890
CC sequences.
XX
SQ Sequence 3441 BP; 966 A; 711 C; 820 G; 944 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.81e-35 Length: 3441
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADF42056 (1-3441)
QY 1 GluAlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
Db 901 GAGGCTTGAATCTTCCATGTGTAGAGGTCCATGTATGCTTTCTCCCAAGATGGGCT 960
QY 21 PheAspAlaValIleGlyGlyCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40
Db 961 TTCATGCTGTATAGGTAAGTGTGTTTGTTCCTATAGTGTGTTGTCAAGATAAGGT 1020
QY 41 AsnIysPheTyrSerGluIleGlyCysArgGlyIleTyrCysGlyValPro 56
Db 1021 AACAGTCTACTCTGAAAGGAATGTAGAGATATCTGTGGTTCCA 1068
RESULT 18
ADP42068 standard; DNA; 3444 BP.
XX
AC ADF42068;
XX
DT 12-FEB-2004 (first entry)
XX
DE Plasmid pDB2301X-derived DPI-14-(GGS) 4GG-rHA-(GGS) 4GG-DX-890 fusion DNA.
XX
KW albumin fusion; Kunitz domain; cytosolic; haemostatic;
KW hereditary angioedema; cancer; bleeding; gene therapy; plasmid pDB2301X;
KW ds; DPI-14-(GGS) 4GG-rHA-(GGS) 4GG-DX-890 fusion; gene.
XX
OS Synthetic.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 829..3090
FT /*tag= a
FT /product= "Plasmid pDB2301X-derived DPI-14-(GGS) 4GG-rHA-
FT (GGS) 4GG-DX-890 fusion precursor protein"
XX
PW MO2003066824-A2.
XX
PD 14-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-US003616.
XX

PR 07-FEB-2002; 2002US-0355547P.
XX
XX (AVET) AVENTIS BEHRING GMBH.
PA (AVET) AVENTIS BEHRING LLC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (DYXN-) DYAX CORP.
XX
PI Hauser H, Wetmer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;
XX
DR WPI: 2003-731497/69.
DR P-PSDB; ADF42028.
XX
PT Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
PS Example 22; Page 66-68; 110pp; English.
XX
CC The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates a
CC cytosolic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the plasmid pDB2301X-derived DPI-14-(GGS) 4GG-rHA-
CC (GGS) 4GG-DX-890 fusion DNA of the invention. NOTE: This sequence also
CC contains regions of cDNA.
XX
SQ Sequence 3444 BP; 968 A; 713 C; 819 G; 944 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.82e-35 Length: 3444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
XX
US-10-038-722-27 (1-56) x ADF42068 (1-3444)
QY 1 GluAlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
Db 2920 GAGGCTTGCATCTTCCATGCTCCGTGCGCTTGCATCGCTTTTCTCCTGCGGCC 2979
QY 21 PheAspAlaValIleGlyGlyCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40
Db 2980 TTTGACGCGCTCAAGGCAATGCGTCTTTTCTTACGCGGCTTGCACAGGCAATGGC 3039
QY 41 AsnIysPheTyrSerGluIleGlyCysArgGlyIleTyrCysGlyValPro 56
Db 3040 AATAAATTTTATAGCGAAGAAAGAGTCCGTGATGTTGCGGCGCTTCT 3087
RESULT 19
ADR90019 standard; DNA; 3444 BP.
XX
AC ADR90019;
XX
DT 18-NOV-2004 (first entry)
XX
DE DPI-14-(GGS) 4 GG-rHA-(GGS) 4 GG-DX-890 fusion DNA.
XX
KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytosolic; haemostatic; human; rHA synthase gene; human albumin; HA;
KW DPI-14; DX-890; chimeric; gene; ds.
XX
OS Homo sapiens.
OS Chimeric.
OS Unidentified.
OS

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XX Key Location/Qualifiers
FH CDS 829..3090
FT /tag= b
FT /product= "DPI-14- (GGS) 4 GG-rHA- (GGS) 4 GG-DX-890 fusion
FT protein"
FT sig_peptide 829..900
FT /tag= a
FT /note= "Fusion leader sequence"
FT CDS 901..3090
FT /tag= d
FT /product= "Mature DPI-14- (GGS) 4 GG-rHA- (GGS) 4 GG-DX-890
FT fusion protein"
FT misc_feature 901..1080
FT /tag= c
FT /note= "DPI-14 CDNA"
FT misc_feature 1081..1121
FT /tag= e
FT /note= "GS linker region"
FT misc_feature 1122..2877
FT /tag= f
FT /note= "rHA synthase gene"
FT misc_feature 2878..2918
FT /tag= g
FT /note= "GS linker region"
FT misc_feature 2919..3087
FT /tag= h
FT /note= "DX-890 DNA"
FH US2004171794-A1.
FH 02-SEP-2004.
PD 07-FEB-2003; 2003US-00361997.
PR 07-FEB-2003; 2003US-00361997.
XX (LADN/) LADNER R C.
PA (LEYA/) LEY A C.
XX LADNER RC, LEY AC;
PI WPI; 2004-625120/60.
DR P-PSDB; ADR90020, ADR90021.
XX New Kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
XX Example 22; SEQ ID NO 44; 123pp; English.
XX The invention relates to proteins comprising kunitz domain peptide,
XX designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX albumin. The invention is useful for treating cystic fibrosis and related
XX diseases, hereditary angioedema, cancer and related diseases including
XX chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX cystostatic and haemostatic agent. The present sequence is a DPI-14-(GGS) 4
XX GG-rHA- (GGS) 4 GG-DX-890 fusion DNA. This fusion DNA contains DPI-14 CDNA,
XX GS linker region, rHA (human albumin) synthase gene and DX-890 CDNA. This
XX sequence is used in the exemplification of the invention.
SQ Sequence 3444 BP; 968 A; 713 C; 819 G; 944 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4,82e-35 Length: 3444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-038-722-27 (1-56) x ADR90019 (1-3444)

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OY 1 GluAlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 22920 GAGGCTTGCAATCTTCCATCGTCGTCGCGCCCTTGCAATCGCCTTTTCTCGTGGGCC 2979
OY 21 PheAspAlaValIleVgGlyVgCysValLeuPheProTrpArgGlyCysGlnGlyAsnGly 40
DB 2980 TTGACGCGCGTCAAGGCAAAATGCGTCTTTTCTTACGGCGGTGCGACGGCAATGGC 3039
OY 41 AsnIysPheTrpSerGluIleVgGlyCysArgGlyIleTrpCysGlyValPro 56
DB 3040 AATTAATTTTATACGCAAGAAAGATGCGGTGATGATTCGCGCGTCCCT 3087
RESULT 20
AAT35166
ID AAT35166 standard; DNA; 8584 BP.
AC AAT35166;
XX 14-FEB-1997 (first entry)
XX DE Plasmid pHL-D2 (MfalpnaPrePro::EPI-HNE-3).
XX KM Apractinin; Kunitz domain; human neutrophil elastase; hNE;
XX KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
XX KW alpha1 antitrypsin; respiratory disorder; cystic fibrosis;
XX KW smokers emphysema; ds.
XX OS Synthetic.
FH Key Location/Qualifiers
FH CDS 954..1379
FT /tag= a
FT /product= "EPI-HNE-3 modified Kunitz domain"
FH MO9620278-A2.
FH 04-JUL-1996.
PD 15-DEC-1995; 95WO-US016349.
PR 16-DEC-1994; 94US-00358160.
XX (PROT-) PROTEIN ENG CORP.
PA Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
PI WPI; 1996-321851/32.
XX New engineered inhibitors of human neutrophil elastase - contg. apractinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
XX respiratory disorders.
XX Example 10; Page 68-73; 105pp; English.
XX Genetically engineered human derived Kunitz domains can be used to
XX inhibit human neutrophil elastase, an enzyme involved in the elimination
XX of pathogens and the restructuring of connective tissue. In cases of
XX reduction of the circulating alpha-1-protease inhibitor (API or alpha1
XX antitrypsin), or the inactivation of API by oxidation (smokers
XX emphysema), extensive destruction of the lung tissue may result from
XX uncontrolled elastolytic activity of human neutrophil elastase. Other
XX respiratory disorders such as cystic fibrosis are thought to be caused by
XX human neutrophil elastase release by neutrophils. The genetically
XX engineered human derived Kunitz domains can be used to treat such
XX respiratory disorders. See AAR99146-R99211. Fusion genes were used in the
XX production of the Kunitz domain derivatives. Protein expression cassettes
XX are then cloned into the plasmid pHL-D2 using BamBI and EcoRI
XX restriction sites. The cloned sequence is under the transcriptional
XX control of Pichia pastoris axol gene promoter and regulatory sequences
XX and downstream polyadenylation and transcription termination sequences.
XX Transformed strains of P. pastoris were used to express the various EPI-
XX HNE proteins derived from the BPT1 and ITT-D2 Kunitz domains. This
XX sequence comprises pHL-D2 having an EPI-HNE-3 Kunitz domain expression

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CC cassette inserted into it. It was designated PHIL-D2 (MfalpabPrePro::Epi-
CC HNE-3)
XX
SQ Sequence 8584 BP; 2264 A; 2024 C; 1976 G; 2320 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 7,86e-34 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AAT35166 (1-8584)
QY 2 AlaCysaenLeuProIleValaIArgGlyProCysIleAlaPhePheProArgTTPalaPhe 21
Db 1212 GCTTGTAACCTGGCCATGCTCAGAGGTCATGATGCTTCTTCCCAAGATGGGCTTTC 1271
QY 22 AspAlaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyVal 41
Db 1272 GACGCTGTTAAGGGTAAGTGGCTTGTTCCTCCATACGGTGGTGTGTCAGATACGGTAC 1331
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 1332 AAGTTCTACTCTGAGAAGAGGTAGAGATCTGTGTTCCA 1376
RESULT 21
AAT35168 ID AAT35168 standard; DNA; 8590 BP.
XX AC AAT35168;
XX DT 14-FEB-1997 (first entry)
XX DE Plasmid pD2pick (MfalpabPrePro::Epi-HNE-3).
XX KM Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
XX KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
XX KM alpha antitrypsin; respiratory disorder; cystic fibrosis;
XX KM smokers emphysema; ds.
XX OS Synthetic.
XX FT Key Location/Qualifiers
FT CDS 954..1379
FT /tag= a
FT /product= "EPI-HNE-3 modified Kunitz domain"
XX PN MO9620278-A2.
XX PD 04-JUL-1996.
XX PF 15-DEC-1995; 95WO-US016349.
XX PR 16-DEC-1994; 94US-00358160.
XX PA (PROT-) PROTEIN ENG CORP.
XX PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX DR MPI; 1996-321851/32.
XX DR P-PSDB; AAR99214.
XX PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin
XX PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
XX PT respiratory disorders.
XX BS Example 10; Page 76-81; 105BP; English.
XX CC Genetically engineered human derived Kunitz domains can be used to
XX CC inhibit human neutrophil elastase, an enzyme involved in the elimination
XX CC of pathogens and the restructuring of connective tissue. In cases of

CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211. Fusion genes were used in the
CC production of the Kunitz domain derivatives. Protein expression cassettes
CC are then cloned into the plasmid PHIL-D2 using BamBI and EcoRI
CC restriction sites. The cloned sequence is under the transcriptional
CC control of Pichia pastoris axo1 gene promoter and regulatory sequences
CC and downstream polyadenylation and transcription termination sequences.
CC Transformed strains of P. pastoris were used to express the various Epi-
CC HNE proteins derived from the BpTI and IPI-D2 Kunitz domains. This
CC sequence comprises PHIL-D2 having an Epi-HNE-3 Kunitz domain expression
CC cassette inserted into it. It was designated pD2pick (MfalpabPrePro::Epi-
CC HNE-3). This sequence differs from the sequence given in AAT35166 by
CC having had two restriction sites, one BamBI and one AatII site, removed
CC from the sequence. This means that the Kunitz domain encoding segment is
CC bounded by unique AatII and EcoRI sites
SQ Sequence 8590 BP; 2265 A; 2026 C; 1972 G; 2321 T; 0 U; 6 Other;
Alignment Scores:
Pred. No.: 7,87e-34 Length: 8590
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AAT35166 (1-8590)
QY 2 AlaCysaenLeuProIleValaIArgGlyProCysIleAlaPhePheProArgTTPalaPhe 21
Db 1212 GCTTGTAACCTGGCCATGCTCAGAGGTCATGATGCTTCTTCCCAAGATGGGCTTTC 1271
QY 22 AspAlaValIysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyVal 41
Db 1272 GACGCTGTTAAGGGTAAGTGGCTTGTTCCTCCATACGGTGGTGTGTCAGATACGGTAC 1331
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 1332 AAGTTCTACTCTGAGAAGAGGTAGAGATCTGTGTTCCA 1376
RESULT 22
AAT79078 ID AAT79078 standard; DNA; 204 BP.
XX AC AAT79078;
XX DT 11-NOV-1997 (first entry)
XX DE Anti-trypsin inhibitor UTI Kunitz domain 2 coding sequence.
XX KM Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
XX KM neutrophil; disease; modification; site directed mutagenesis; ss.
XX OS Homo sapiens.
XX PN JP09124700-A.
XX PD 13-MAY-1997.
XX PF 07-NOV-1995; 95JP-00288527.
XX PR 07-NOV-1995; 95JP-00288527.
XX PA (GREC) GREEN CROSS CORP.
XX DR MPI; 1997-316576/29.
XX DR P-PSDB; AAW25930.

XX New protease inhibitor - useful for treating diseases involving elastase.
PT
XX
PS Disclosure; Page 24; 37pp; Japanese.
XX
XX This is the nucleotide sequence encoding the anti-trypsin inhibitor UTI
CC Kunitz domain 2. The nucleotide sequence was used to construct a novel
CC protease inhibitor in which the active site residues of the Kunitz domain
CC 1 (M5929) are substituted (see AAT79080, AAT79081 and AAT79083). The
CC modified protease inhibitors are targeted to the protease elastase,
CC especially from neutrophils and can be used to treat diseases associated
CC with elastase. Modifications of the active site were done by site
CC directed mutagenesis
SQ Sequence 204 BP; 37 A; 56 C; 67 G; 44 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.7e-32 Length: 204
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AAT79078 (1-204)
QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 10 GCATGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATT 69
QY 22 AspAlaValIleGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGTCAAGGGAAGTGGCTCTTCCCTACGGGGGCTGCACAGGCAACGGGAAC 129
QY 42 LysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTGGGGTGTCCCT 174
RESULT 23
AAV40045
ID AAV40045 standard; cDNA to mRNA; 204 BP.
AC AAV40045;
DT 09-NOV-1998 (first entry)
DE UTI cDNA SEQ ID NO:27 from WO9829453 Example 13.
KW Drug; cell membrane-directed drug; phospholipid; lipid bilayer;
KW cell cortex; blood coagulation; inflammation; immunological disorder; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..204
FT /*tag= a
FT /note= "no stop codon given"
XX
XX WO9829453-A1.
XX
XX 09-JUL-1998.
XX
XX 05-JAN-1998; 98WO-JP000002.
XX
XX 27-DEC-1996; 96JP-00359053.
XX
XX (MOCH) MOCHIDA PHARM CO LTD.
XX
XX Kuriyama S, Hasegawa T;
XX
XX WPI; 1998-388051/33.
XX
XX P-PSDB; AAM69521.
XX

XX
XX Drugs containing peptide(s) with specific affinity to phospholipid(s) -
PT such as phosphatidyl serine, for treatment of blood coagulation,
PT inflammatory and immunological disorders.
XX
XX Example 13; Page 83; 117pp; Japanese.
XX
XX The present invention describes drug compositions which contain as an
CC active component a peptide which has specific affinity to particular
CC phospholipids (such as phosphatidyl ethanolamine or phosphatidyl serine),
CC especially to phospholipid which constitute a lipid bilayer of cellular
CC cortex and of which the concentration in the bilayer increases in cells
CC which are abnormal (e.g. through injury, denaturation or activation). In
CC particular, the peptide contains a sequence having phospholipid affinity
CC and a structure of formula (I): (A1)a-(A2)b-(A3)c, where (A1) is one of
CC two specific sequences (see AAM69516 and AAM69519), (A2) and (A3) are
CC TRVLRHPSQSWHQLALR, LRVLRHPSQSWHQLALR (see AAM69517) or MEVLGCEAQLLY
CC (see AAM69518); a = 0-5; b = 1-5, and c = 0-5. Preferred are the formulae
CC A1-A2-A3, A2-A3, A2-A2-A3, A2-A2-A2-A3 or A2-A2 (especially A2-A2-A3, A2-
CC A2-A2-A3 or A2-A2). The sequence is linked to a peptide such as a blood
CC factor, especially thrombo-modulin, urina-statin or membrane cofactor
CC protein. The drugs are used for the treatment and prevention of diseases
CC involving blood coagulation, inflammatory and immunological disorders.
CC The present sequence encodes a protein from the present invention
XX
SQ Sequence 204 BP; 37 A; 59 C; 65 G; 43 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.7e-32 Length: 204
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AAV40045 (1-204)
QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 4 GCCTGCATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATT 63
QY 22 AspAlaValIleGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 64 GATGCTGTCAAGGGAAGTGGCTCTTCCCTACGGGGGCTGCACAGGCAACCGGAAC 123
QY 42 LysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56
DB 124 AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTGGGGTGTCCCT 168
RESULT 24
AAQ78607
ID AAQ78607 standard; DNA; 210 BP.
AC AAQ78607;
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
DE DNA sequence downstream of DNA encoding E. coli alkaline phosphatase.
KW fusion protein; protein expression; secretion; alkaline phosphatase;
KW recombinant DNA technology; signal peptide; Escherichia coli; ss.
XX
XX Synthetic.
OS
XX
XX EP624644-A1.
XX
XX 17-NOV-1994.
XX
XX 29-APR-1994; 94EP-00106773.
XX
XX 01-MAY-1993; 93JP-00128528.
XX
XX

PA (MOCH) MOCHIDA PHARM CO LTD.
 XX Morishita H, Kanamori T, Nobuhara M;
 XX WPI: 1994-350784/44.
 DR P-PSDB; AAR65481.
 XX
 PT Vector contg. a DNA fragment - used to produce a protein of interest.
 PS
 XX Example 3; Page 15; 65bp; English.
 XX
 CC AAQ78607 is a nucleotide sequence which is downstream of a nucleotide
 CC sequence that encodes E. coli alkaline phosphatase signal peptide. It
 CC encodes the protein shown in AAR65476. Plasmid pM594, used for the
 CC expression of AN68 (sic) (see AAR65478), was constructed from plasmid
 CC pM552 which contains a tryptophan promoter, a Kanamycin resistant gene
 CC and also AAQ78607. The vectors for the expression of AN68, each contain a
 CC nucleotide sequence of general formula: j-x-y-z (j = AAQ78606; x =
 CC AAQ78598/078601; y = a nucleotide sequence that encodes Met; and z
 CC represents the nucleotide sequence that encodes AN68). When a protein of
 CC interest is expressed as a fusion protein contg. 'x' (encoded by x) its
 CC expression and/or secretion quantity increases. (Updated on 25-MAR-2003
 CC to correct PN field.)
 CC
 XX Sequence 210 BP; 38 A; 63 C; 65 G; 44 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 4,88e-32 Length: 210
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 2 Gaps: 0
 US-10-038-722-27 (1-56) x AAQ78607 (1-210)
 QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
 DB 10 GCCTGCAATCTCCCATAGTCCGGGGCCCTCCGAGCTTCATCAGCTCGGGCATTT 69
 QY 22 AspAlaValIlyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 70 GATGCTGTCAAGGGAAGTGCCTCTCCCTACGGGGGCTGCAGGGGCAACGGGAAC 129
 QY 42 LysPheTyrSerGluLysGluCysArgGlyLysGlyValPro 56
 DB 130 AAGTTCTACTCAGAGAAGAGTGCAGAGACTGCGGTGTCCT 174
 RESULT 25
 AAQ64758
 ID AAQ64758 standard; DNA; 210 BP.
 XX
 AC AAQ64758;
 XX
 DT 10-MAR-2003 (revised)
 DT 27-JUN-1994 (first entry)
 XX
 DE Protease inhibitor gene #3.
 XX
 KM Protease inhibitor; core region; dyspnea disease of adult; allergy;
 KM polycystic failure; shock; pancreatitis; chronic articular rheumatism;
 KM intravascular coagulation disease; operation invasion; arthritis; se.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FH misc_feature 1..9
 FT /tag= a
 FT /note= "May be serially deleted by multiples of 3 bp"
 FT misc_feature 13..165
 FT /tag= b
 FT /note= "Wild type core region"

FT misc_feature 169..210
 FT /tag= c
 FT /note= "May be serially deleted by multiples of 3 bp"
 XX
 XX JP05308988-A.
 XX
 XX 22-NOV-1993.
 XX PD
 XX 12-MAY-1992; 92JP-00146587.
 XX PF
 XX 12-MAY-1992; 92JP-00146587.
 XX PR
 XX 12-MAY-1992; 92JP-00146587.
 XX
 PA (MOCH) MOCHIDA PHARM CO LTD.
 XX
 DR WPI: 1994-002180/01.
 DR P-PSDB; AAR54721.
 XX
 PT New polypeptide - useful for prevention and therapy of diseases related
 PT to protease e.g. pancreatitis.
 XX
 PS Claim 11 and 12; Page 3; 27pp; Japanese.
 XX
 CC The sequences given in AAQ64756-59 are DNA sequences encoding extended
 CC versions of a wild type core polypeptide which acts as a protease
 CC inhibitor. The peptides encoded by these sequences may also contain
 CC deletions within the core region (see also AAQ64751-55). These deletions
 CC lead to the production of peptides with enhanced protease inhibitor
 CC action. These peptides may be used for the prevention and therapy of
 CC diseases related to protease, such as operation invasion, polycystic
 CC failure, shock, pancreatitis, intravascular coagulation disease, dyspnea
 CC disease of adult, chronic articular rheumatism, arthritis or allergy.
 CC (Updated on 10-MAR-2003 to add missing OS field.)
 XX
 SQ Sequence 210 BP; 40 A; 60 C; 65 G; 45 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4,88e-32 Length: 210
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 2 Gaps: 0
 US-10-038-722-27 (1-56) x AAQ64758 (1-210)
 QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
 DB 10 GCCTGTAATCTACCAATAGTCCGGGGCCCTCCGAGCTTCATCAGCTCGGGCATTT 69
 QY 22 AspAlaValIlyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 DB 70 GATGCTGTCAAGGGAAGTGCCTCTCCCTACGGGGGCTGCAGGGGCAACGGGAAC 129
 QY 42 LysPheTyrSerGluLysGluCysArgGlyLysGlyValPro 56
 DB 130 AAGTTCTACTCAGAGAAGAGTGCAGAGACTGCGGTGTCCT 174

Search completed: February 23, 2005, 04:36:01
 Job time : 395 secs

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OM protein - protein search, using sw model

Run on: February 23, 2005, 03:27:40 ; Search time 63 Seconds
(without alignments)
290.881 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPYRGPCIAFFPRWA.....QGNNGKFKYSEKREYCGVP 56

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	56	14	US-10-038-722-27 = LLLFV
2	329	100.0	56	15	US-10-456-986A-49 = LLLFV
3	329	100.0	56	16	US-10-361-997-40 = LL
4	329	100.0	141	14	US-10-038-722-74
5	329	100.0	655	16	US-10-361-997-59
6	329	100.0	655	16	US-10-361-997-61
7	329	100.0	694	16	US-10-361-997-71
8	329	100.0	728	16	US-10-361-997-75
9	329	100.0	729	16	US-10-361-997-46
10	329	100.0	752	16	US-10-361-997-74
11	329	100.0	753	16	US-10-361-997-45
12	324	98.5	56	14	US-10-038-722-26 = LLLFV
13	324	98.5	56	15	US-10-456-986A-47 = LLLFV

14	324	98.5	56	15	US-10-456-986A-48 = LLLFV	Sequence 48, App1
15	324	98.5	141	14	US-10-038-722-72 = LLLFV	Sequence 72, App1
16	324	98.5	141	14	US-10-038-722-76 = LLLFV	Sequence 76, App1
17	296	90.0	57	10	US-09-974-026-26 = LL	Sequence 26, App1
18	296	90.0	57	10	US-10-167-351-78 = LL	Sequence 28, App1
19	296	90.0	58	14	US-10-038-722-25	Sequence 25, App1
20	296	90.0	58	15	US-10-456-986A-31	Sequence 28, App1
21	296	90.0	58	16	US-10-361-997-8	Sequence 31, App1
22	296	90.0	68	15	US-10-298-796-23	Sequence 8, App1
23	296	90.0	147	14	US-10-038-722-77	Sequence 23, App1
24	296	90.0	147	15	US-10-298-796-24	Sequence 77, App1
25	296	90.0	352	15	US-10-291-172-281	Sequence 24, App1
26	296	90.0	352	15	US-10-291-265-450	Sequence 281, App
27	296	90.0	352	15	US-10-291-265-922	Sequence 450, App
28	296	90.0	352	15	US-10-221-278-281	Sequence 922, App
29	296	90.0	366	9	US-09-925-301-1175	Sequence 281, App
30	294	89.4	58	14	US-10-167-351-131	Sequence 1175, App
31	294	89.4	58	16	US-10-361-997-20	Sequence 131, App
32	294	89.4	61	10	US-09-896-095-171	Sequence 20, App1
33	294	89.4	61	14	US-10-038-722-114	Sequence 171, App
34	294	89.4	61	15	US-10-115-134-28	Sequence 114, App
35	287	87.2	58	14	US-10-167-351-130	Sequence 28, App1
36	285	86.6	58	14	US-10-167-351-132	Sequence 130, App
37	272	82.7	61	10	US-09-896-095-178	Sequence 132, App
38	272	82.7	61	14	US-10-038-722-121	Sequence 178, App
39	272	82.7	61	15	US-10-115-134-35	Sequence 121, App
40	271	82.4	58	14	US-10-167-351-79	Sequence 35, App1
41	261	79.3	58	14	US-10-167-351-133	Sequence 79, App1
42	221	67.2	58	14	US-10-038-722-63	Sequence 133, App
43	216	65.7	58	14	US-10-038-722-57	Sequence 63, App1
44	203	61.7	58	14	US-10-038-722-67	Sequence 57, App1
45	201	61.1	58	14	US-10-038-722-37	Sequence 67, App1
						Sequence 37, App1

ALIGNMENTS

RESULT 1
US-10-038-722-27

Sequence 27, Application US/10038722
Publicatoin No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Epi-HNE-4
US-10-038-722-27

Query Match 100.0%; Score 329; DB 14; Length 56;
Best local Similarity 100.0%; Pred. No. 2.7e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 EACNLPYRGPCIAFFPRWADAVKGCVLFPYGGCQGNKFKYSEKREYCGVP 56

Db 1 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 2
US-10-456-986A-49
; Sequence 49, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hiranil, Shrish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epl-HNE-4 Sequence
US-10-456-986A-49

Query Match 100.0%; Score 329; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.7e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
Db 1 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 3
US-10-361-997-40
; Sequence 40, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-10-361-997-40

Query Match 100.0%; Score 329; DB 16; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.7e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
Db 1 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 4

US-10-038-722-74
; Sequence 74, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BacBI-AclII-EcoRI cassette for expression of Epl-HNE-4 (Table 252
US-10-038-722-74

Query Match 100.0%; Score 329; DB 14; Length 141;
Best Local Similarity 100.0%; Pred. No. 6.7e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
Db 86 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 141

RESULT 5
US-10-361-997-59
; Sequence 59, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the N-terminal
; OTHER INFORMATION: DX-890-(GGG)4GG-albumin fusion protein
US-10-361-997-59

Query Match 100.0%; Score 329; DB 16; Length 655;
Best Local Similarity 100.0%; Pred. No. 3.1e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
Db 1 EACNLPYVGPCTIAFPFPMADAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 6
US-10-361-997-61
; Sequence 61, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the C-terminal
US-10-361-997-61

Query Match 100.0%; Score 329; DB 16; Length 655;
Best Local Similarity 100.0%; Pred. No. 3.1e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMAPDAVKGKCVLPYGGCGGNGNKFYSEKCREYCGVP 56
Db 600 EACNLPYRGPCIAFPFPMAPDAVKGKCVLPYGGCGGNGNKFYSEKCREYCGVP 555

RESULT 7
US-10-361-997-71
; Sequence 71, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence encoded by NotI cassette of
; OTHER INFORMATION: pDB2300X2 with DX890 (Nterm) and Cterm linker
US-10-361-997-71

Query Match 100.0%; Score 329; DB 16; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.3e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMAPDAVKGKCVLPYGGCGGNGNKFYSEKCREYCGVP 56
Db 25 EACNLPYRGPCIAFPFPMAPDAVKGKCVLPYGGCGGNGNKFYSEKCREYCGVP 80

RESULT 8
US-10-361-997-75
; Sequence 75, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles

; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of
; OTHER INFORMATION: DX-890:::(GGS)4GG:::HA:::(GGS)4GG:::DX890
US-10-361-997-75

Query Match 100.0%; Score 329; DB 16; Length 728;
Best Local Similarity 100.0%; Pred. No. 3.4e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMAPDAVKGKCVLPYGGCGGNGNKFYSEKCREYCGVP 56
Db 1 EACNLPYRGPCIAFPFPMAPDAVKGKCVLPYGGCGGNGNKFYSEKCREYCGVP 56

RESULT 9
US-10-361-997-46
; Sequence 46, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Secreted product
US-10-361-997-46

Query Match 100.0%; Score 329; DB 16; Length 729;
Best Local Similarity 100.0%; Pred. No. 3.5e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EACNLPYRGPCIAFPFPMAPDAVKGKCVLPYGGCGGNGNKFYSEKCREYCGVP 56
Db 674 EACNLPYRGPCIAFPFPMAPDAVKGKCVLPYGGCGGNGNKFYSEKCREYCGVP 729

RESULT 10
US-10-361-997-74
; Sequence 74, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 74
LENGTH: 752
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of NotI cassette of pDB2300X3
US-10-361-997-74

Query Match 100.0%; Score 329; DB 16; Length 752;
Best Local Similarity 100.0%; Pred. No. 3,6e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTAIFPPRPAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 25 EACNLPYVGPCTAIFPPRPAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 80

RESULT 11
US-10-361-997-45
Sequence 45, Application US/10361997
Publication No. US2004017194A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 753
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation product of DPI-14 (GGS) 4
US-10-361-997-45

Query Match 100.0%; Score 329; DB 16; Length 753;
Best Local Similarity 100.0%; Pred. No. 3,6e-32;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTAIFPPRPAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 638 EACNLPYVGPCTAIFPPRPAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 753

RESULT 12
US-10-038-722-26
Sequence 26, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/349,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16

NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Epi-HNE-3
US-10-038-722-26

Query Match 98.5%; Score 324; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTAIFPPRPAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 2 ACNLPYVGPCTAIFPPRPAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 13
US-10-456-986A-47
Sequence 47, Application US/10456986A
Publication No. US20040038893A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert C.
APPLICANT: Ley, Arthur C.
APPLICANT: HIRANI, Shrish
APPLICANT: WILLIAMS, Anthony
TITLE OF INVENTION: Prevention and Reduction of Blood Loss
FILE REFERENCE: 3421.1001-002
CURRENT APPLICATION NUMBER: US/10/456,986A
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/387,239
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/407,003
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EPI-HNE-2 Sequence
US-10-456-986A-47

Query Match 98.5%; Score 324; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTAIFPPRPAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 2 ACNLPYVGPCTAIFPPRPAFDVAVKGCYLPFYGGCGGNGNKFYSEKREYCGVP 56

RESULT 14
US-10-456-986A-48
Sequence 48, Application US/10456986A
Publication No. US20040038893A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert C.
APPLICANT: LEY, Arthur C.
APPLICANT: HIRANI, Shrish
APPLICANT: WILLIAMS, Anthony
TITLE OF INVENTION: Prevention and Reduction of Blood Loss
FILE REFERENCE: 3421.1001-002
CURRENT APPLICATION NUMBER: US/10/456,986A
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/387,239
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/407,003
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 54


```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPI-HNE-3 Sequence
US-10-456-986A-48

Query Match          98.5%; Score 324; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56

RESULT 15
US-10-038-722-72
; Sequence 72, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pHIL-D2 (Mfalphaprepro:EPI-HNE-3) (Table 251)
US-10-038-722-72

Query Match          98.5%; Score 324; DB 14; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.8e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 87 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 141

RESULT 16
US-10-038-722-76
; Sequence 76, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
```

```
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPI-HNE-3 fusion protein (Table 253)
US-10-038-722-76

Query Match          98.5%; Score 324; DB 14; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.8e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 87 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 141

RESULT 17
US-09-974-026-26
; Sequence 26, Application US/09974026
; Publication No. US20030194398A1
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P
; APPLICANT: Davis, Gary
; APPLICANT: Delaria, Katherine A
; APPLICANT: Christopher, Marlor W
; APPLICANT: Daniel, Miller K
; TITLE OF INVENTION: Human Btkunin
; FILE REFERENCE: 96-223-Z2
; CURRENT APPLICATION NUMBER: US/09/974,026
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 09/144,428
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: PCT/US97/03894
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 08/725,251
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: US 60/019,793
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: US 60/013,106
; PRIOR FILING DATE: 1996-03-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Kunitz-like domain of inter-alpha-trypsin inhibitor precursor.
US-09-974-026-26

Query Match          90.0%; Score 296; DB 10; Length 57;
Best Local Similarity 92.7%; Pred. No. 3.4e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 56
Db 3 ACNLPYVGPCLAFPPRMAFDVAVKGCYLPFYGGCGGNGNKFYSKECREYCGVP 57

RESULT 18
US-10-167-351-78
; Sequence 78, Application US/10167351
; Publication No. US20030165896A1
; GENERAL INFORMATION:
```

```
APPLICANT: DYAX CORP.
APPLICANT: Markland, William
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
FILE REFERENCE: DYX-007.2P US-4
CURRENT APPLICATION NUMBER: US/10/167,351
PRIOR FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 09/638,770
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 09/114,878
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/240,136
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 08/676,124
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: PCT/US95/00298
PRIOR FILING DATE: 1995-01-11
PRIOR APPLICATION NUMBER: 08/208,265
PRIOR FILING DATE: 1994-03-10
PRIOR APPLICATION NUMBER: 08/179,658
PRIOR FILING DATE: 1994-01-11
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 78
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-10-167-351-78
```

```
Query Match          90.0%; Score 296; DB 14; Length 58;
Best Local Similarity 92.7%; Pred. No. 3.5e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 56
DB 4 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 58
```

RESULT 19

```
US-10-038-722-25
Sequence 25, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-722-25
```

```
Query Match          90.0%; Score 296; DB 14; Length 58;
Best Local Similarity 92.7%; Pred. No. 3.5e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 56
DB 4 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 58
```

```
DB 4 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 58
```

```
RESULT 20
US-10-456-986A-31
Sequence 31, Application US/10456986A
Publication No. US20040038893A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert C.
APPLICANT: Ley, Arthur C.
APPLICANT: Hiran, Shrish
APPLICANT: Williams, Anthony
TITLE OF INVENTION: Prevention and Reduction of Blood Loss
FILE REFERENCE: 3421.1001-002
CURRENT APPLICATION NUMBER: US/10/456,986A
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 60/387,239
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/407,003
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 58
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ITI-D2 Sequence
US-10-456-986A-31
```

```
Query Match          90.0%; Score 296; DB 15; Length 58;
Best Local Similarity 92.7%; Pred. No. 3.5e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 56
DB 4 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 58
```

RESULT 21

```
US-10-361-997-8
Sequence 8, Application US/10361997
Publication No. US20040171794A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-10-361-997-8
```

```
Query Match          90.0%; Score 296; DB 16; Length 58;
Best Local Similarity 92.7%; Pred. No. 3.5e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 56
DB 4 ACNLPYVGPCLAFPPRMAFDVAVKGCYLFPYGGCGGNGNKFYSKECREYCGVP 58
```

```
RESULT 22
US-10-298-796-23
Sequence 23, Application US/10298796
Publication No. US20030220490A1
```

```

; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-298-796-23

Query Match          90.0%; Score 296; DB 15; Length 68;
Best Local Similarity 92.7%; Pred. No. 4e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56

RESULT 23
US-10-038-722-77
; Sequence 77, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: IT1-D1 KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY-18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-722-77

Query Match          90.0%; Score 296; DB 14; Length 147;
Best Local Similarity 92.7%; Pred. No. 8.7e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 81 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 135

RESULT 24
US-10-298-796-24
; Sequence 24, Application US/10298796
; Publication No. US20030220490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
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; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-298-796-24

Query Match          90.0%; Score 296; DB 15; Length 147;
Best Local Similarity 92.7%; Pred. No. 8.7e-29;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 81 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 135

RESULT 25
US-10-291-172-281
; Sequence 281, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030228584A1el Nucleic acids and polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 281
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-281

Query Match          90.0%; Score 296; DB 15; Length 352;
Best Local Similarity 92.7%; Pred. No. 2.1e-28;
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 286 ACNLPYVGPCTIAFPFRWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 340

Search completed: February 23, 2005, 03:31:47
Job time : 63 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 23, 2005, 03:29:45 ; Search time 39 Seconds
(without alignments)
60.358 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329

Sequence: 1 EACNLPYIRGPCIAPFFPRWA.....QGNKNKFSKREYCGVP 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169943 seqs, 42035171 residues

Total number of hits satisfying chosen parameters: 169943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	182	55.3	576	7	US-11-028-058-7
2	182	55.3	640	7	US-11-028-058-5
3	176	53.5	571	7	US-11-028-058-3
4	176	53.5	571	7	US-11-028-058-49
5	172	52.3	548	7	US-11-028-058-11
6	155	47.1	763	1	PCT-US04-42360-1138
7	155	47.1	763	1	PCT-US04-42360-1362
8	155	47.1	765	1	PCT-US04-42360-1136
9	155	47.1	765	1	PCT-US04-42360-1360
10	150	44.6	552	7	US-11-028-058-9
11	146	44.4	547	8	US-60-647-493-4
12	146	44.4	770	6	US-10-287-436A-471
13	146	44.4	770	6	US-10-287-436A-1168
14	146	44.4	770	6	US-10-903-279-2
15	146	44.4	772	6	US-10-450-763-4945
16	146	44.4	1137	6	US-10-450-763-4946
17	144	43.8	195	6	US-10-495-300-28
18	144	43.8	195	6	US-11-050-926-304
19	144	43.8	252	7	US-11-050-926-302
20	140	42.6	841	6	US-10-450-763-50314
21	139	42.2	59	5	US-09-700-179B-46
22	135	41.0	59	5	US-09-700-179B-4
23	135	41.0	60	5	US-09-700-179B-11
24	135	41.0	83	5	US-09-700-179B-18
25	135	41.0	83	5	US-09-700-179B-57

26	133	40.4	59	5	US-09-700-179B-2	Sequence 2, Appli
27	133	40.4	83	5	US-09-700-179B-16	Sequence 15, Appl
28	133	40.4	83	5	US-09-700-179B-55	Sequence 16, Appl
29	133	40.4	3176	6	US-10-852-335A-160	Sequence 160, App
30	133	40.4	3176	6	US-10-287-436A-503	Sequence 503, App
31	133	40.4	3176	6	US-10-287-436A-1196	Sequence 1196, App
32	132	40.1	59	5	US-09-700-179B-47	Sequence 47, Appl
33	129	39.2	235	7	US-11-050-926-316	Sequence 316, Appl
34	127	38.6	88	6	US-10-485-231-26	Sequence 26, Appl
35	126	38.3	62	5	US-09-700-179B-48	Sequence 48, Appl
36	122	37.1	59	5	US-09-700-179B-6	Sequence 6, Appli
37	122	37.1	60	5	US-09-700-179B-53	Sequence 53, Appl
38	122	37.1	83	5	US-09-700-179B-20	Sequence 20, Appl
39	122	37.1	83	5	US-09-700-179B-59	Sequence 59, Appl
40	117	35.6	83	5	US-09-700-179B-65	Sequence 65, Appl
41	115	35.0	130	1	PCT-US05-02350-369	Sequence 369, App
42	115	35.0	130	7	US-11-043-770-369	Sequence 369, App
43	115	35.0	164	5	US-09-999-570A-96	Sequence 96, Appl
44	115	35.0	225	1	PCT-US05-02350-368	Sequence 368, App
45	115	35.0	225	7	US-11-043-770-368	Sequence 368, App

ALIGNMENTS

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RESULT 1
US-11-028-058-7
Sequence 7, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 7
LENGTH: 576
TYPE: PRT
ORGANISM: Homo sapiens
US-11-028-058-7

Query Match      55.3%   Score 182; DB 7; Length 576;
Best Local Similarity 52.7%; Pred. No. 7; Le-16;
Matches 29; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY      2 ACNLPYIRGPCIAPFFPRWAQDAVYKCYLFPYGGQGNKFSKREYCGVP 56
DB      365 ACSLPALGQPCAKAVAPRAVYNSQTGQCSFYGGGEGGNFSEACEESCFFP 439

RESULT 2
US-11-028-058-5
Sequence 5, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645

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PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 640
TYPE: PRT
ORGANISM: Homo sapiens
US-11-028-058-5

Query Match 53.3%; Score 182; DB 7; Length 640;
Best Local Similarity 52.7%; Pred. No. 7.9e-16;
Matches 29; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 ACNLPVIRGPCIAFFPRMAFDVAKGCVLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 449 ACSLPALQGPCAKYVPRMAYNSQTGLQCSFYVGGCGGNGNPFESRACBESCPFP 503

RESULT 3
US-11-028-058-3
Sequence 3, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: WOLFMAN, NEIL M.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 571
TYPE: PRT
ORGANISM: Mus sp.
US-11-028-058-3

Query Match 53.5%; Score 176; DB 7; Length 571;
Best Local Similarity 51.9%; Pred. No. 4.2e-15;
Matches 28; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 3 CNLPVIRGPCIAFFPRMAFDVAKGCVLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 381 CSLPPLQGPCAKYVPRMAYNSQTGLQCSFYVGGCGGNGNPFESRACBESCPFP 434

RESULT 4
US-11-028-058-49
Sequence 49, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: WOLFMAN, NEIL M.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 571
TYPE: PRT
ORGANISM: Mus sp.

US-11-028-058-49

Query Match 53.5%; Score 176; DB 7; Length 571;
Best Local Similarity 51.9%; Pred. No. 4.2e-15;
Matches 28; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 3 CNLPVIRGPCIAFFPRMAFDVAKGCVLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 381 CSLPPLQGPCAKYVPRMAYNSQTGLQCSFYVGGCGGNGNPFESRACBESCPFP 434

RESULT 5
US-11-028-058-11
Sequence 11, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: WOLFMAN, NEIL M.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 548
TYPE: PRT
ORGANISM: Homo sapiens
US-11-028-058-11

Query Match 52.3%; Score 172; DB 7; Length 548;
Best Local Similarity 50.0%; Pred. No. 1.3e-14;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 EACNLPVIRGPCIAFFPRMAFDVAKGCVLPFYGGCGGNGNKFYSEKREYCGVP 56
DB 357 DACVLPVAVQGPCRGEPRMAYNSPLTQCHPFPYVGGCGGNGNPFESRACBACFPV 412

RESULT 6
PCT-US04-42360-1138
Sequence 1138, Application PC/TUS0442360
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: 17633/2048
CURRENT APPLICATION NUMBER: PCT/US04/42360
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: 60/531,341
PRIOR FILING DATE: 19-Dec-2003
NUMBER OF SEQ ID NOS: 2587
SOFTWARE: Perl script
SEQ ID NO 1138
LENGTH: 763
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Refseq / NP_057244
DATABASE ENTRY DATE: 2003-10-04
PCT-US04-42360-1138

Query Match 47.1%; Score 155; DB 1; Length 763;
Best Local Similarity 54.9%; Pred. No. 3.1e-12;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

QY 3 CNLPVIRGPCIAFFPRMAFDVAKGCVLPFYGGCGGNGNKFYSEKREYCGVP 53
DB 357 DACVLPVAVQGPCRGEPRMAYNSPLTQCHPFPYVGGCGGNGNPFESRACBACFPV 412

Db 310 CSOAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNNNFESSEEDYCMAYC 360

RESULT 7

PCT-US04-42360-1362
; Sequence 1362, Application PCT/US0442360
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; PRIOR FILING DATE: 19-Dec-2003
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script
; SEQ ID NO 1362
; LENGTH: 763
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_057244
; DATABASE ENTRY DATE: 2003-10-04
PCT-US04-42360-1362

Query Match 47.1%; Score 155; DB 1; Length 763;
Best Local Similarity 54.9%; Pred. No. 3.1e-12;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Qy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCULFPYGGCGGNGKFKYSEKREYIC 53
Db 310 CSOAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNNNFESSEEDYCMAYC 360

RESULT 8

PCT-US04-42360-1136
; Sequence 1136, Application PCT/US0442360
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; PRIOR FILING DATE: 19-Dec-2003
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script
; SEQ ID NO 1136
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / M11322
; DATABASE ENTRY DATE: 2003-02-28
PCT-US04-42360-1136

Query Match 47.1%; Score 155; DB 1; Length 765;
Best Local Similarity 54.9%; Pred. No. 3.1e-12;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Qy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCULFPYGGCGGNGKFKYSEKREYIC 53
Db 312 CSOAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNNNFESSEEDYCMAYC 362

RESULT 9

PCT-US04-42360-1360
; Sequence 1360, Application PCT/US0442360
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG

; TITLE OF INVENTION: Nucleotide sequences involved in pain

; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; PRIOR FILING DATE: 19-Dec-2003
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script
; SEQ ID NO 1360
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / M11322
; DATABASE ENTRY DATE: 2003-02-28
PCT-US04-42360-1360

Query Match 47.1%; Score 155; DB 1; Length 765;
Best Local Similarity 54.9%; Pred. No. 3.1e-12;
Matches 28; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

Qy 3 CMLPIVRGPCIAFFPRMAFDVAVKGCULFPYGGCGGNGKFKYSEKREYIC 53
Db 312 CSOAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNNNFESSEEDYCMAYC 362

RESULT 10

US-11-028-058-9
; Sequence 9, Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: MOLEMAN, NEIL M.
; TITLE OF INVENTION: POLYSTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-9

Query Match 45.6%; Score 150; DB 7; Length 552;
Best Local Similarity 42.9%; Pred. No. 9.8e-12;
Matches 24; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy 1 EACNLPYVRGPCIAFFPRMAFDVAVKGCULFPYGGCGGNGKFKYSEKREYIC 56
Db 361 DVICALPVGCPGCGMERRMAISPLLOQCHPRIVYSGCEBNSNFTRESCEBACPVF 416

RESULT 11

US-60-647-493-4
; Sequence 4, Application US/60647493
; GENERAL INFORMATION:
; APPLICANT: Rubinstein, Amy
; TITLE OF INVENTION: TRANSGENIC ZEBRAFISH MODELS FOR
; FILE REFERENCE: 26007.0004U1
; CURRENT APPLICATION NUMBER: US/60/647,493
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 547

Qy 1 EACNLPIVGPICIAFFPRMAFDVKGKCVLPFYGGCGGNGNKFYSEKREYCG 54
| : | | | | | | | | | | : | |
Db 289 EVVSEQAEETGPCRAMISRWFVTEGKCAPFYGGCGGNGNRNFPDTEETCAVCG 342

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Job time : 40 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:30:15 ; Search time 2610 Seconds
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Title: US-10-038-722-27
329
Sequence: 1 EACNLPIYRGCIAFPFRA.....QGNKFKYSEKREYCVGP 56

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 45554873 segs, 20411521753 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 12: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
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- 22: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
- 26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
- 27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*

- 29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
- 33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
- 34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
- 35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
- 36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
- 37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
- 38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq:*
- 39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
- 40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
- 41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
- 42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
- 43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:*
- 44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq:*
- 45: /cgn2_6/ptodata/1/pna/US099G_COMB.seq:*
- 46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
- 47: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
- 48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq:*
- 49: /cgn2_6/ptodata/1/pna/US101B_COMB.seq:*
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- 52: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
- 53: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:*
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- 55: /cgn2_6/ptodata/1/pna/US104B_COMB.seq:*
- 56: /cgn2_6/ptodata/1/pna/US105A_COMB.seq:*
- 57: /cgn2_6/ptodata/1/pna/US105B_COMB.seq:*
- 58: /cgn2_6/ptodata/1/pna/US105B_COMB.seq:*
- 59: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:*
- 60: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
- 61: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:*
- 62: /cgn2_6/ptodata/1/pna/US107D_COMB.seq:*
- 63: /cgn2_6/ptodata/1/pna/US108A_COMB.seq:*
- 64: /cgn2_6/ptodata/1/pna/US108B_COMB.seq:*
- 65: /cgn2_6/ptodata/1/pna/US108B_COMB.seq:*
- 66: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
- 67: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
- 68: /cgn2_6/ptodata/1/pna/US110_COMB.seq:*
- 69: /cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
- 70: /cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
- 71: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:*
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- 75: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
- 76: /cgn2_6/ptodata/1/pna/US6007_COMB.seq:*
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- 78: /cgn2_6/ptodata/1/pna/US6009_COMB.seq:*
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- 80: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
- 81: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
- 82: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
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- 84: /cgn2_6/ptodata/1/pna/US6015_COMB.seq:*
- 85: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
- 86: /cgn2_6/ptodata/1/pna/US6017_COMB.seq:*
- 87: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
- 88: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
- 89: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
- 90: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
- 91: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
- 92: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq:*
- 93: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq:*
- 94: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
- 95: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
- 96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
- 97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
- 98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
- 99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
- 100: /cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
- 101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	329	100.0	190	US-10-361-997-57	Sequence 57, Appl
2	329	100.0	195	US-10-361-997-56	Sequence 56, Appl
3	329	100.0	207	US-10-361-997-72	Sequence 72, Appl
4	329	100.0	444	US-08-849-406-73	Sequence 73, Appl
5	329	100.0	444	US-10-038-722-73	Sequence 73, Appl
6	329	100.0	1965	US-10-361-997-58	Sequence 58, Appl
7	329	100.0	1965	US-10-361-997-60	Sequence 60, Appl
8	329	100.0	3255	US-10-361-997-70	Sequence 70, Appl
9	329	100.0	3440	US-10-361-997-73	Sequence 73, Appl
10	329	100.0	3444	US-10-361-997-44	Sequence 44, Appl
11	329	100.0	8584	US-08-849-406-71	Sequence 71, Appl
12	329	100.0	8584	US-10-038-722-71	Sequence 71, Appl
13	329	100.0	8584	US-08-849-406-75	Sequence 75, Appl
14	329	100.0	8590	US-08-849-406-75	Sequence 75, Appl
15	329	100.0	8590	US-08-849-406-75	Sequence 75, Appl
16	329	100.0	8590	US-08-849-406-75	Sequence 75, Appl
17	329	100.0	198	US-08-293-150-12	Sequence 12, Appl
18	329	100.0	204	US-10-298-796-27	Sequence 27, Appl
19	329	100.0	204	US-10-298-796-27	Sequence 27, Appl
20	329	100.0	204	US-10-298-796-27	Sequence 27, Appl
21	329	100.0	209	US-08-293-150-15	Sequence 15, Appl
22	329	100.0	210	US-08-293-150-11	Sequence 11, Appl
23	329	100.0	210	US-08-293-150-11	Sequence 11, Appl
24	329	100.0	275	US-09-534-840-4698	Sequence 4698, Ap
25	329	100.0	295	US-08-293-150-85	Sequence 85, Appl
26	329	100.0	313	US-08-293-150-75	Sequence 75, Appl
27	329	100.0	322	US-09-321-214-27983	Sequence 27983, A
28	329	100.0	322	US-09-516-335-27983	Sequence 27983, A
29	329	100.0	322	US-09-733-811-27983	Sequence 27983, A
30	329	100.0	322	US-09-733-811-27983	Sequence 27983, A
31	329	100.0	322	US-09-975-640-27983	Sequence 27983, A
32	329	100.0	322	US-09-975-640-27983	Sequence 27983, A
33	329	100.0	333	US-09-515-128-23052	Sequence 23052, A
34	329	100.0	333	US-09-721-544-23052	Sequence 23052, A
35	329	100.0	343	US-08-235-515-28	Sequence 28, Appl

36 296 90.0 350 8 US-08-293-150-92 Sequence 92, Appl
 37 296 90.0 408 18 US-09-235-076-8710 Sequence 8710, Ap
 38 296 90.0 408 18 US-09-248-797-28240 Sequence 28240, A
 39 296 90.0 408 20 US-09-332-782-8710 Sequence 8710, Ap
 40 296 90.0 408 33 US-09-737-223-8710 Sequence 8710, Ap
 41 296 90.0 408 39 US-09-918-995-8710 Sequence 8710, Ap
 42 296 90.0 408 40 US-09-925-564-28240 Sequence 28240, A
 43 296 90.0 435 19 US-09-287-618-17842 Sequence 17842, A
 44 296 90.0 441 51 US-10-298-796-28 Sequence 28, Appl
 45 296 90.0 441 51 US-10-298-796B-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
 US-10-361-997-57
 ; Sequence 57, Application US/10361997
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert Charles
 ; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
 ; FILE REFERENCE: 3421.1015-000
 ; CURRENT FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: US 60/355,547
 ; PRIOR FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 57
 ; LENGTH: 190
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: DNA sequence of the C-Terminal BamHI-HindIII
 ; OTHER INFORMATION: DX-890 cDNA
 ; US-10-361-997-57

Alignment Scores:
 Pred. No.: 5,45e-34 Length: 190
 Score: 329.00 Matches: 56
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Gaps: 0
 DB: 53 Indels: 0

US-10-038-722-27 (1-56) x US-10-361-997-57 (1-190)
 QY 1 GUAAGCCTGTAATCTGCAATGTTAGAGTCCATGTTCTTCCCAAGATGGCT 20
 DB 13 GAAGCCTGTAATCTGCAATGTTAGAGTCCATGTTCTTCCCAAGATGGCT 72
 QY 21 PHEAPPAVALLYSGLYLVCYVALLEUPHEPOTRYSGLYCYSGGLGGLYASGLY 40
 DB 73 TTCAGTGTGTTAAGGTAAGTGTGTTGTTCCATAGGTTGTTGTAAGGTAAGCT 132
 QY 41 AenlyspheTYserGLyGLyGLyCYsArGLyurYCYsGLyValPro 56
 DB 133 AACAACTTCTACTCGAAGGAATGTAGAGATATCTGTGTTCCA 180

RESULT 2
 US-10-361-997-56
 ; Sequence 56, Application US/10361997
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert Charles
 ; APPLICANT: Ley, Arthur C.
 ; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
 ; FILE REFERENCE: 3421.1015-000
 ; CURRENT FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: US 60/355,547
 ; PRIOR FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 56
LENGTH: 195
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA sequence of the N-Terminal BglII-BamHI DX-890
US-10-361-997-56

Alignment Scores:
Pred. No.: 5.63e-34 Length: 195
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-56 (1-195)

Qy 1 GUAUACySaAnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
Db 19 GAAGCTTGAATCTTCCATGTTAGAGTCCATGATTTCTTTCCCAAGATGGCT 78

Qy 21 PheAspAlaValIyGlyLysCysValLeuPheProTyrgIyGlyCysGlnGlyAsnGly 40
Db 79 TTCATGCTGTTAAGGTAAGTGTGTTTGTCCATATGGTGGTGTCAAGATAAGGT 138

Qy 41 AsnLysPheTyrsSerGluLysGluCysArgGluTyrcysGlyValPro 56
Db 139 AACAAATTACTCTGAAGAAAGATGAGAAATCTGTGTGTTCCA 186

RESULT 3
US-10-361-997-72
Sequence 72, Application US/10361997
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421, 1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 207
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA to insert at BspEI/KpnI site for 2nd encoding
US-10-361-997-72

Alignment Scores:
Pred. No.: 6.05e-34 Length: 207
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-72 (1-207)

Qy 1 GUUAUACySaAnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
Db 28 GAGGCTTGAATCTTCTATCGTCGCGCTTCATGCGCTTTTCTCTCGTGGGCC 87

Qy 21 PheAspAlaValIyGlyLysCysValLeuPheProTyrgIyGlyCysGlnGlyAsnGly 40
Db 88 TTTGACGCGTGAAGGCAATGCGTCTTTTCTTCCATGCGGTGGCCAGGCAATGAC 147

Qy 41 AsnLysPheTyrsSerGluLysGluCysArgGluTyrcysGlyValPro 56

Db 148 AATAAATTATATGCGAGAAAGATGCGGTAGATATGCGGCTCCCT 195

RESULT 4
US-08-849-406-73
Sequence 73, Application US/08849406
APPLICANT: Ley, Arthur C.
LADNER, Robert C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCE: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-08-849-406-73

Alignment Scores:
Pred. No.: 1.53e-33 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-038-722-27 (1-56) x US-08-849-406-73 (1-444)

Qy 1 GUUAUACySaAnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
Db 265 GAGGCTTGAATCTTCCATGTTAGAGTCCATGATTTCTTTCCCAAGATGGCT 324

Qy 21 PheAspAlaValIyGlyLysCysValLeuPheProTyrgIyGlyCysGlnGlyAsnGly 40
Db 325 TTCACGCTGTTAAGGTAAGTGTGTTTCCATATGGTGGTGTCAAGATAAGGT 384

Qy 41 AsnLysPheTyrsSerGluLysGluCysArgGluTyrcysGlyValPro 56
Db 385 AACAAATTACTCTGAAGAAAGATGAGAAATCTGTGTGTTCCA 432

RESULT 5
US-08-849-406A-73
Sequence 73, Application US/08849406A
APPLICANT: LEY, Arthur C.
LADNER, Robert C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEWMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406A
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-08-849-406A-73
Alignment Scores:
Pred. No.: 1.53e-33 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-038-722-27 (1-56) x US-08-849-406A-73 (1-444)
QY 1 GIUAlaCyAsnLeuProIleValaLagIyProCySIlleAlaPhePheProArGTTPaLa 20
DB 265 GAGGCTTGAACCTTGCAATCGCAGAGGTGCATGCAATGCTTTCTTCCCAAGATGGGCT 324
QY 21 PheAspAlaValIlyGlyGlyCySValIleuPheProTyGlyGlyCySGInglyAsngly 40
DB 325 TTCGACGCTTAAAGGCTAAGTCCGCTTCTTCCCATACGGTGGTGTGTCAAGGTAAACGGT 384
QY 41 AenIysPheTySerGluIyGlyGlyCySArGluTyCySGIlyValPro 56
DB 385 AACAGTTTACTCTGAGAAGAGGTGTAGAGAGTACTGTGTGTCCA 432
RESULT 6
US-10-038-722-73
Sequence 73, Application US/10038722

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
FILE REFERENCE: LEY-1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patent version 3.1
SEQ ID NO 73
LENGTH: 444
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: BclBI-AatII-EcoRI cassette for expression of Epl-HNE-4 (Table 252
US-10-038-722-73
Alignment Scores:
Pred. No.: 1.53e-33 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 46 Gaps: 0
US-10-038-722-27 (1-56) x US-10-038-722-73 (1-444)
QY 1 GIUAlaCyAsnLeuProIleValaLagIyProCySIlleAlaPhePheProArGTTPaLa 20
DB 265 GAGGCTTGAACCTTGCAATCGCAGAGGTGCATGCAATGCTTTCTTCCCAAGATGGGCT 324
QY 21 PheAspAlaValIlyGlyGlyCySValIleuPheProTyGlyGlyCySGInglyAsngly 40
DB 325 TTCGACGCTTAAAGGCTAAGTCCGCTTCTTCCCATACGGTGGTGTGTCAAGGTAAACGGT 384
QY 41 AenIysPheTySerGluIyGlyGlyCySArGluTyCySGIlyValPro 56
DB 385 AACAGTTTACTCTGAGAAGAGGTGTAGAGAGTACTGTGTGTCCA 432
RESULT 7
US-10-361-997-58
Sequence 58, Application US/10361997
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58
LENGTH: 1965
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA sequence of the N-Terminal
OTHER INFORMATION: DX-890-(GGG)4GG-albumin fusion coding region
US-10-361-997-58

Alignment Scores:
Pred. No.: 9,41e-33 Length: 1965
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-58 (1-1965)

QY 1 GIUAlaCySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 1 GAAGCCTGTAATCTTCCCAATGTAGAGGTCCATGATGCTTCTTCCCAAGATGGCT 60

QY 21 PheAspAlaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 61 TTCGATGCTTTAAGGTAAGTGTGTTGTTCCCATATGAGTGTGTCACAGGTAAAGCT 120

QY 41 AsnIysPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56
DB 121 AACAGTCTACTCTGAAGAAAGTAAGTAAGATCTGTGTTCCA 168

RESULT 8
US-10-361-997-60
; Sequence 60, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of the C-terminal
; OTHER INFORMATION: albumin-(GGS) 4GG-DX-890 fusion coding region
US-10-361-997-60

Alignment Scores:
Pred. No.: 9,41e-33 Length: 1965
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-60 (1-1965)

QY 1 GIUAlaCySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 1798 GAAGCCTGTAATCTTCCCAATGTAGAGGTCCATGATGCTTCTTCCCAAGATGGCT 1857

QY 21 PheAspAlaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 1858 TTCGATGCTTTAAGGTAAGTGTGTTGTTCCCATATGAGTGTGTCACAGGTAAAGCT 1917

QY 41 AsnIysPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56
DB 1918 AACAGTCTACTCTGAAGAAAGTAAGTAAGATCTGTGTTCCA 1965

RESULT 9
US-10-361-997-70
; Sequence 70, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.

; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 3255
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NotI cassette of pDB2300X2 with DX890 (Nterm) and
; OTHER INFORMATION: Cerm linker ready for second DX890
US-10-361-997-70

Alignment Scores:
Pred. No.: 1,74e-32 Length: 3255
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-70 (1-3255)

QY 1 GIUAlaCySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
DB 901 GAAGCCTGTAATCTTCCCAATGTAGAGGTCCATGATGCTTCTTCCCAAGATGGCT 960

QY 21 PheAspAlaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 961 TTCGATGCTTTAAGGTAAGTGTGTTGTTCCCATATGAGTGTGTCACAGGTAAAGCT 1020

QY 41 AsnIysPheTyrSerGlyLysGlyCysArgGlyTyrCysGlyValPro 56
DB 1021 AACAGTCTACTCTGAAGAAAGTAAGTAAGATCTGTGTTCCA 1068

RESULT 10
US-10-361-997-73
; Sequence 73, Application US/10361997
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 3440
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of NotI cassette of pDB2300X3 with 2
; OTHER INFORMATION: x DX-890
US-10-361-997-73

Alignment Scores:
Pred. No.: 1,86e-32 Length: 3440
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 53 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-73 (1-3440)

QY 1 GIUAlaCySaenLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/849,406A
APPLICATION NUMBER: US/08/849,406A
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 8584 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-08-849-406A-71

Alignment Scores:
Pred. No.: 2,65e-31 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 14 Gaps: 0
US-10-038-722-27 (1-56) x US-08-849-406A-71 (1-8584)
QY 2 AlaCysAsnLeuProIleValAlaArgGlyProCysIleAlaPheProAlaPhe 21
DB 1212 GCTGTAACTTCCCAATGCTCAGAGTCCATGCTTTCTTCCCAAGATGGCTTTC 1271
QY 22 AspaIaValIysGlyIysCysValIeuPheProTyrGlyIysCysGlnGlyAsnGlyAsn 41
DB 1272 GACGCTGTAAGGTAAGTGGCTTGTTCATACGGGTGTGTCAGAGTAACGTAAC 1331
QY 42 LysPheTyrSerGluIysGluCysArgGlyTyrCysGlyValPro 56
DB 1332 AAGTCTACTCTGAGAGAGAGTGAAGAGTACTGTGTGCCA 1376

RESULT 14
US-10-038-722-71
Sequence 71, Application US/10038722
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
FILE REFERENCE: LEY=1B
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.1
SEQ ID NO 71
LENGTH: 8584

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid pHI1-D2 (MpaIhapPrepro::EPI-HNE-3) (Table 251)
US-10-038-722-71

Alignment Scores:
Pred. No.: 2,65e-31 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 14 Gaps: 0
US-10-038-722-27 (1-56) x US-10-038-722-71 (1-8584)
QY 2 AlaCysAsnLeuProIleValAlaArgGlyProCysIleAlaPheProAlaPhe 21
DB 1212 GCTGTAACTTCCCAATGCTCAGAGTCCATGCTTTCTTCCCAAGATGGCTTTC 1271
QY 22 AspaIaValIysGlyIysCysValIeuPheProTyrGlyIysCysGlnGlyAsnGlyAsn 41
DB 1272 GACGCTGTAAGGTAAGTGGCTTGTTCATACGGGTGTGTCAGAGTAACGTAAC 1331
QY 42 LysPheTyrSerGluIysGluCysArgGlyTyrCysGlyValPro 56
DB 1332 AAGTCTACTCTGAGAGAGAGTGAAGAGTACTGTGTGCCA 1376

RESULT 15
US-08-849-406-75
Sequence 75, Application US/08849406
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,406
FILING DATE: 21-Jul-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16349
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8590 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 75;
US-08-849-406-75

Alignment Scores:
Pred. No.: 2,65e-31 Length: 8590
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 14 Gaps: 0

US-10-038-722-27 (1-56) x US-08-849-406-75 (1-8590)

Qy	2	AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe	21
Db	1212	GCTTGTAACCTTCCCAATCCTCAGAGGTCATGCAATTCCTTCTCCCAAGATGGGCTTTC	1271
Qy	22	AspAlaValIleGlyLysCysValLeuPheProTyrGlyCysGlnGlyAsnGlyAsn	41
Db	1272	GACGCTTAAGGGTAAGTGGCTGTTCCCATACGGGTGTGTCAAGTAAAGGTAAAC	1331
Qy	42	LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro	56
Db	1332	AAGTCTACTCTGAGAGGAGGTAGAGTACTGTGTGTTCCA	1376

Search completed: February 23, 2005, 04:19:26
Job time : 2615 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:30:45 ; Search time 591 Seconds

(without alignments)
61.077 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPIVRGPCIAFPFPRMA.....QGNGKFKYSEKREYCVGP 56

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 5167335 seqs, 322287606 residues

Total number of hits satisfying chosen parameters: 10334670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPFO.spool/US10038722/runat_18022005_145204_14132/app_query.fasta.1.199
-DB=Pending Patents NA_New -QFMT=fastap -SUFFIX=trnp -MINMATCH=0.1 -LOOFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10038722_QCGN_1_1_228@runat_18022005_145204_14132 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESOURCE -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA_New:*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US12_NEW_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	296	90.0	1436	7	US-10-485-231-7
2	182	55.3	1731	8	US-11-028-058-6
3	182	55.3	1923	8	US-11-028-058-4
4	176	53.5	1716	8	US-11-028-058-1
5	176	53.5	1716	8	US-11-028-058-2
6	176	53.5	1716	8	US-11-028-058-48
7	176	52.3	1695	8	US-11-028-058-10
8	155	47.1	3727	1	PCT-US04-42360-1137
9	155	47.1	3727	1	PCT-US04-42360-1361

10	150	45.6	1659	8	US-11-028-058-8	Sequence 8, Appli
11	146	44.4	669	7	US-10-287-436A-1006	Sequence 1006, Ap
12	146	44.4	3414	6	US-10-450-763-19078	Sequence 19078, A
13	146	44.4	3579	6	US-10-287-436A-118	Sequence 118, App
14	146	44.4	3585	7	US-10-450-763-19077	Sequence 19077, A
15	144	43.8	1509	6	US-10-495-300-27	Sequence 27, Appli
16	144	43.8	1544	8	US-11-050-926-301	Sequence 301, App
17	144	43.8	1558	8	US-11-050-926-103	Sequence 301, App
18	141.5	43.0	3238	7	US-10-450-763-19079	Sequence 19079, A
19	135	41.0	180	5	US-09-700-179B-3	Sequence 3, Appli
20	135	41.0	180	5	US-09-700-179B-50	Sequence 50, Appli
21	135	41.0	252	5	US-09-700-179B-17	Sequence 17, Appli
22	135	41.0	252	5	US-09-700-179B-58	Sequence 58, Appli
23	134	40.7	4069	7	US-10-450-763-19946	Sequence 19946, A
24	133	40.4	180	5	US-09-700-179B-15	Sequence 15, Appli
25	133	40.4	252	5	US-09-700-179B-15	Sequence 15, Appli
26	133	40.4	252	5	US-09-700-179B-56	Sequence 56, Appli
27	133	40.4	10558	6	US-10-852-335A-66	Sequence 66, Appli
28	133	40.4	10558	6	US-10-287-436A-151	Sequence 151, App
29	133	40.4	10558	6	US-10-287-436A-764	Sequence 764, App
30	129	39.2	1142	8	US-11-050-926-115	Sequence 315, App
31	127	38.6	941	7	US-10-485-231-25	Sequence 25, Appli
32	123	37.4	408	5	US-09-700-179B-43	Sequence 43, Appli
33	123	37.4	408	5	US-09-700-179B-54	Sequence 54, Appli
34	122	37.1	180	5	US-09-700-179B-5	Sequence 52, Appli
35	122	37.1	252	5	US-09-700-179B-19	Sequence 19, Appli
36	122	37.1	252	5	US-09-700-179B-60	Sequence 60, Appli
37	122	37.1	252	5	US-09-700-179B-60	Sequence 349, App
38	115	35.0	148	1	PCT-US05-02350-349	Sequence 349, App
39	115	35.0	148	1	US-11-043-770-349	Sequence 349, App
40	115	35.0	1252	1	PCT-US05-02350-342	Sequence 342, App
41	115	35.0	1252	1	US-11-043-770-342	Sequence 342, App
42	115	35.0	1294	5	US-09-999-570A-47	Sequence 47, Appli
43	115	35.0	1307	5	US-09-999-570A-95	Sequence 95, Appli
44	115	35.0	1309	1	PCT-US05-02350-343	Sequence 343, App
45	115	35.0	1309	8	US-11-043-770-343	Sequence 343, App

ALIGNMENTS

RESULT 1
US-10-485-231-7
; Sequence 7, Application US/10485231
; GENERAL INFORMATION:
; APPLICANT: GENSET
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 142.WO1
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 60/311,305
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/314,734
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/318,204
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/326,470
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..263
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 264..926
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 927..1436
; FEATURE:

```

NAME/KEY: polYA_signal
LOCATION: 1404..1409
FEATURE:
NAME/KEY: polYA_site
LOCATION: 1421..1436
US-10-485-231-7

Alignment Scores:
Pred. No.: 2,33e-29      Length: 1436
Score: 296.00           Matches: 51
Percent Similarity: 92.73%  Conservative: 0
Best Local Similarity: 92.73%  Mismatches: 4
Query Match: 89.97%       Indels: 0
DB: 7                    Gaps: 0

US-10-038-722-27 (1-56) x US-10-485-231-7 (1-1436)

Oy 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
Db 1117 GCCTGCATCTCTCCCATATGATCGGGGCCCTTCGCGAGCCTTATCTACACTCTGGGACATT 1176

Oy 22 AspaValAlValysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 1177 GATGCTGCACAGGGGAGATGGGTCTTCTTCCCTTACGGGGGGCTGCGACAGGCAACGGCAAC 1236

Oy 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 1237 AAGTTCTACTCAGAGAGAGAGTGCAGAGACTGCGGTGTCCTT 1281

RESULT 2
Sequence 6, Application US/11028058
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: MOLEMAN, NEIL M.
TITLE OF INVENTION: FOLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702, 0015-00
CURRENT APPLICATION NUMBER: US/11/028,058
PRIOR FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1731
TYPE: DNA
ORGANISM: Homo sapiens
US-11-028-058-6

Alignment Scores:
Pred. No.: 4.47e-14      Length: 1731
Score: 182.00           Matches: 29
Percent Similarity: 70.91%  Conservative: 10
Best Local Similarity: 52.73%  Mismatches: 16
Query Match: 55.32%       Indels: 0
DB: 8                    Gaps: 0

US-10-038-722-27 (1-56) x US-11-028-058-6 (1-1731)

Oy 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
Db 1153 GCCTGCACACTCTCCCGCCCTGCGAGGGGCCCTTCGCAAGCTTACGCGCCTTCGCGGCTTAC 1212

Oy 22 AspaValAlValysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 1213 AACAGCCAGACGGGCGCAGTGCAGTCTTGTCTATGATGGCTGCGAGGCGCATATGCAAC 1272

Oy 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
Db 1237 AAGTTCTACTCAGAGAGAGAGTGCAGAGACTGCGGTGTCCTT 1281

```

```

Db      1273 AACCTTGAGAGCCGTGAGGCGCTGTGAGAGAGTGTGCGCCCTTCC 1317

RESULT 3
US-11-028-058-4
; Sequence 4, Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT FILING DATE: 2005-01-04
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (732)
; OTHER INFORMATION: a, t, c or g
US-11-028-058-4

Alignment Scores:
Pred. No.:          5,07e-14          Length:          1923
Score:              182.00             Matches:          29
Percent Similarity: 70.91%             Conservative:     10
Best Local Similarity: 52.73%           Mismatches:      16
Query Match:        55.32%             Indels:           0
DB:                 8                  Gaps:            0

US-10-038-722-27 (1-56) x US-11-028-058-4 (1-1923)

QY      2 A1aCysaenleupProIleValaArgIlyProCysIleAlaPheProArgTrpAlaPhe 21
Db      1345 GCGTGCAGCCTGCCCGCCGCTGCAGGGGCGCCGCAAAAGCTTACGGCGCTGAGGCTTAC 140
QY      22 AspAlaValIlySGIlyLysCysValleupheProTyrIgtIlyGlyCysGInglyAsnGlyAsn 41
Db      1405 AACAGCCAGACGGCGCAGTGCAGTCTTGTCTATGTGTGCTGCGAGGGCAATGGCAAC 146
QY      42 LysheTyrSerGluIlyGluCysArgIlyTyrCysGlyValPro 56
Db      1465 AACCTTGAGAGCCGTGAGGCGCTGTGAGAGAGTGTGCGCCCTTCC 1509

RESULT 4
US-11-028-058-1
; Sequence 1, Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT FILING DATE: 2005-01-04
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1716
; TYPE: DNA

```

```
US-11-028-058-1
```

ORGANISM: Mus sp.
US-11-028-058-1

Alignment Scores:
Pred. No.: 2,78e-13 Length: 1716
Score: 176.00 Matches: 28
Percent Similarity: 68.52% Conservative: 9
Best Local Similarity: 51.85% Mismatches: 17
Query Matchn: 53.50% Indels: 0
DB: Gaps: 0

US-10-038-722-27 (1-56) x US-11-028-058-1 (1-1716)

OY 3 CysAsnLeuProlIleValArgGlyProCysIleAlaPhePheProArGTTPAlaPheasp 22
Db 1141 TGCAGCCCTGCCCTTCACAAAGGGCGTTGCAAAAGCTTATGTGCCAAGCTGGAGCTTACCAC 1200
OY 23 AlalValLysGIyLySCysValLeuPheProTYrGIyGIyCSySnglYAASngLYAAnLyS 42
Db 1201 AGCCAGACAGGCGCTATGCCAGTCTTCTGCTATGGCGGCTGTGAGGGCAACGTAACAAC 1260
OY 43 PheTYrSerGIuLySGluCYsArgGLuTYrCYsgILyValPro 56
Db 1261 TTtGAAGAAGCCGTGAGGCTTGAGAGAGTGTGTCCCTTCCCG 1302

RESULT 5
US-11-028-058-2

/ Sequence 2, Application US/11028058
/ GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: WOLFMAN, NEIL M.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
FILE REFERENCE: 08702.0015-00
CURRENT APPLICATION NUMBER: US/11/028_058
PRIOR FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/10/369,736
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 60/357,846
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/434,645
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1716
TYPE: DNA
ORGANISM: Mus sp.
US-11-028-058-2

Alignment Scores:
Pred. No.: 2,78e-13 Length: 1716
Score: 176.00 Matches: 28
Percent Similarity: 68.52% Conservative: 9
Best Local Similarity: 51.85% Mismatches: 17
Query Matchn: 53.50% Indels: 0
DB: Gaps: 0

US-10-038-722-27 (1-56) x US-11-028-058-2 (1-1716)

OY 3 CysAsnLeuProlIleValArgGlyProCysIleAlaPhePheProArGTTPAlaPheasp 22
Db 1141 TGCAGCCCTGCCCTTCACAAAGGGCGTTGCAAAAGCTTATGTGCCAAGCTGGAGCTTACCAC 1200
OY 23 AlalValLysGIyLySCysValLeuPheProTYrGIyGIyCSySnglYAASngLYAAnLyS 42
Db 1201 AGCCAGACAGGCGCTATGCCAGTCTTCTGCTATGGCGGCTGTGAGGGCAACGTAACAAC 1260
OY 43 PheTYrSerGIuLySGluCYsArgGLuTYrCYsgILyValPro 56
Db 1261 TTtGAAGAAGCCGTGAGGCTTGAGAGAGTGTGTCCCTTCCCG 1302

RESULT 6
US-11-028-058-48

```

; Sequence 48 Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028, 058
; PRIOR FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369, 736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357, 846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434, 645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1713)
US-11-028-058-48

Alignment Scores:
Pred. No.: 2,78e-13 Length: 1716
Score: 176.00 Matches: 28
Percent Similarity: 68.52% Conservative: 9
Best Local Similarity: 51.85% Mismatches: 17
Query Match: 53.50% Indels: 0
DB: 8 Gaps: 0

US-10-038-722-27 (1-56) x US-11-028-058-48 (1-1716)
QY 3 CysasmeupPcolleVlaRyGlyProCyrtlleAlphePheProAryGTrpAlaPheap 22
DB 1141 TGCAGCTGCTGCTGCCCTGCAGAGGCGCTTGCAAGCTTATGTCCACGCTGGCTTACAC 12000
QY 23 AlavallysGlyLysCysVallePheProTyrglyGlyCysGlnGlyAsnGlyAsnLys 42
DB 1201 AGCCAGACAGGCTTATGCCAGTCCTTGTCTATGCGCGCTGTGAGGCGAAGCTTACAC 12666
QY 43 PheTyrsErgLulysGluCyArGlyLutryCySgLyValPro 56
DB 1261 TTGAAGCGCGTAGGCTTGAGGAGAGTCGTCTCCCTCCG 1302

RESULT 7
US-11-028-058-10
; Sequence 10, Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028, 058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369, 736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357, 846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434, 645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-028-058-10

Alignment Scores:
Pred. No.: 9.35e-13 Length: 1695

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US-10-038-722-27 (1-56) x US-11-028-058-8 (1-1659)
QY      1  GlnAlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
      ::: ||| ||||| |||:::||||| |||::: ||||| |||||
US-10-038-722-27 (1-56) x PCT-US04-42360-1361 (1-3727)
QY      3  CysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPheAsp 22
      ||::: ||::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1000  TGCCTCCAGAGCGGAGTACGCGGCGCTGCGGCGCTGATGCTCGTGTACTTGAC 1059
QY      23  AlaValIysGlyIysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 42
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1060  CTCCTCCAGGGAAGTCCGTCCGCTTATATATGTGTGCTGCGGCGCAACAGAACAT 1159
QY      43  PheTyrSerGluIysGluCysArgGluTyrCys 53
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1120  TTGAGTCTGAGGATTAATGTATGCGCTGTGTGT 1152
RESULT 10
US-11-028-058-8
; Sequence 8, Application US/11028058
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: POLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; PRIOR FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Mus sp.
US-11-028-058-8
Alignment Scores:
Pred. No.: 4,44e-10 Length: 3727
Score: 155.00 Matches: 28
Percent Similarity: 58.82% Conservative: 2
Best Local Similarity: 54.90% Mismatches: 21
Query Match: 47.11% Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-11-028-058-8 (1-1659)
QY      1  GlnAlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAla 20
      ::: ||| ||||| |||:::||||| |||::: ||||| |||||

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Db 1081 GATGTCGTGCACTGCTGCACTGAGGGCCCTGCGAGGGCTGGAGCCAGCTGGGCC 1140
Qy 21 PheaspalaVallyGlyLysCyseValleuPheProTyrglyGlyCyseGlnGlyAsnGly 40
Db 1141 TACAGCCCACTGCTACAGCAGGAGCCACCCCTTTGATACAGTGCGCTGAGAGAAACAGC 1200
Qy 41 AsnlyPheTyrsSerGluLysGluCyseArgGluTyrglyGlyValPro 56
Db 1201 AATACTTTGACACCCGGAGAGCTGTGAGATGCTTCCCTGTACCA 1248

RESULT 11
US-10-287-436A-1006
; Sequence 1006, Application US/10287436A
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1006
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-1006

Alignment Scores:
Pred. No.: 8.88e-10 Length: 669
Score: 146.00 Matches: 26
Percent Similarity: 55.56% Conservative: 4
Best Local Similarity: 48.15% Mismatches: 24
Query Match: 44.38% Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x US-10-287-436A-1006 (1-669)

Qy 1 GluAlaCyseAsnLeuProIleValArgGlyProCyseIleAlaPhePheProArgTrrpAla 20
Db 184 GAGGTGCTCTGACAAAGCCGAGCGGGCCGTCGCCAGCAATGATCTCCCGCTGTAC 243
Qy 21 PheaspalaVallyGlyLysCyseValleuPheProTyrglyGlyCyseGlnGlyAsnGly 40
Db 244 TTTGATGTGACTGAAGGAGAGTGTCCTTTTACGGCGGATGTGGCGGCAACCGG 303
Qy 41 AsnlyPheTyrsSerGluLysGluCyseArgGluTyrglyGlyValPro 54
Db 304 AACCACTTTGACACAGAGAGTACTGATGCGCCGTGTGGC 345

RESULT 12
US-10-450-763-19078
; Sequence 19078, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 19078
; LENGTH: 3414
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1075) .. (1683)
; OTHER INFORMATION: 99% homologous to Homo sapiens APP precursor, accession number
; OTHER INFORMATION: A31584, Smith-Waterman Score=1130.
US-10-450-763-19078

Alignment Scores:
Pred. No.: 6.31e-09 Length: 3414
Score: 146.00 Matches: 26
Percent Similarity: 55.56% Conservative: 4
Best Local Similarity: 48.15% Mismatches: 24
Query Match: 44.38% Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x US-10-450-763-19078 (1-3414)

Qy 1 GluAlaCyseAsnLeuProIleValArgGlyProCyseIleAlaPhePheProArgTrrpAla 20
Db 2266 GAGGTGCTCTGACAAAGCCGAGCGGGCCGTCGCCAGCAATGATCTCCCGCTGTAC 2325
Qy 21 PheaspalaVallyGlyLysCyseValleuPheProTyrglyGlyCyseGlnGlyAsnGly 40
Db 2326 TTTGATGTGACTGAAGGAGAGTGTCCTTTTACGGCGGATGTGGCGGCAACCGG 2385
Qy 41 AsnlyPheTyrsSerGluLysGluCyseArgGluTyrglyGlyValPro 54
Db 2386 AACCACTTTGACACAGAGAGTACTGATGCGCCGTGTGGC 2427

RESULT 13
US-10-287-436A-118
; Sequence 118, Application US/10287436A
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-118

Alignment Scores:
Pred. No.: 6.68e-09 Length: 3579
Score: 146.00 Matches: 26
Percent Similarity: 55.56% Conservative: 4
Best Local Similarity: 48.15% Mismatches: 24
Query Match: 44.38% Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x US-10-287-436A-118 (1-3579)

Qy 1 GluAlaCyseAsnLeuProIleValArgGlyProCyseIleAlaPhePheProArgTrrpAla 20
Db 1012 GAGGTGCTCTGACAAAGCCGAGCGGGCCGTCGCCAGCAATGATCTCCCGCTGTAC 1071
Qy 21 PheaspalaVallyGlyLysCyseValleuPheProTyrglyGlyCyseGlnGlyAsnGly 40
Db 1072 TTTGATGTGACTGAAGGAGAGTGTCCTTTTACGGCGGATGTGGCGGCAACCGG 1131
Qy 41 AsnlyPheTyrsSerGluLysGluCyseArgGluTyrglyGlyValPro 54
Db 1132 AACCACTTTGACACAGAGAGTACTGATGCGCCGTGTGGC 1173

RESULT 14
US-10-450-763-19077
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? NAME/KEY CDS
? LOCATION: 318..902
? FEATURE:
? NAME/KEY: 3'UTR
? LOCATION: 903..1409
? FEATURE:
? NAME/KEY: polyA_signal
? LOCATION: 1345..1350
? FEATURE:
? NAME/KEY: polyA_site
? LOCATION: 1368..1409
US-10-495-300-27

Alignment Scores:
Pred. No.: 4,02e-09 Length: 1409
Score: 144.00 Matches: 26
Percent Similarity: 56.60% Conservative: 4
Best local Similarity: 49.06% Mismatches: 23
Query Match: 43.77% Indels: 0
DB: 6 Gaps: 0

US-10-038-722-27 (1-56) x US-10-495-300-27 (1-1409)

QY 1 GluAlaCYeAsnIeuProlIeValArgGIyProCYsIleAlaPhePheProArgTPAla 20
Db 537 GAATACTGCACCGCCCAACGCACTACTGGGCTTSCCGTGATCATCTTCCACGCTGTAC 596
21 PheaSPALaValIySeGIyLyeCYsValIeuPheProTYrGIyGIyCYsGInGIyAsnGIy 40
QY 21 PheaSPALaValIySeGIyLyeCYsValIeuPheProTYrGIyGIyCYsGInGIyAsnGIy 40
Db 597 TTTCAGCGTGAGAGGAACTCTGCAATTAACCTCATCTATGTAGAGGCTGCCGGGCAATPAG 656
41 AsnIyPheTYrSeGIyLyeGIySeGIyCYsArgGIyTYrCYs 53
QY 41 AsnIyPheTYrSeGIyLyeGIySeGIyCYsArgGIyTYrCYs 53
Db 657 AACAGCTACCGCTCTGAGAGGAGGCTTCGACATGCTCCGCTAC 695

```

Page 6

PA1a 20
|
GTAC 596
|
ngly 40
|
TTAG 656

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 04:29:32 | Search time 1772 Seconds

(without alignments)
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Title: US-10-038-722-27

Perfect score: 329

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5384158 seqs, 2955248155 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications_NA.*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCFUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
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- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	190	US-10-361-997-57	Sequence 57, Appl
2	329	100.0	195	US-10-361-997-56	Sequence 56, Appl
3	329	100.0	207	US-10-361-997-72	Sequence 72, Appl
4	329	100.0	444	US-10-038-722-73	Sequence 72, Appl
5	329	100.0	1965	US-10-361-997-58	Sequence 58, Appl
6	329	100.0	1965	US-10-361-997-60	Sequence 60, Appl
7	329	100.0	3255	US-10-361-997-70	Sequence 70, Appl
8	329	100.0	3444	US-10-361-997-73	Sequence 73, Appl
9	329	100.0	3444	US-10-361-997-74	Sequence 74, Appl
10	324	98.5	8584	US-10-038-722-71	Sequence 44, Appl
11	324	98.5	8590	US-10-038-722-75	Sequence 75, Appl
12	296	90.0	204	US-10-298-796-27	Sequence 27, Appl
13	296	90.0	408	US-09-918-995-8710	Sequence 8710, Ap
14	296	90.0	441	US-10-298-796-28	Sequence 28, Appl
15	296	90.0	1280	US-10-291-265-214	Sequence 214, Ap
16	296	90.0	1436	US-09-978-418-7	Sequence 7, Appl
17	296	90.0	1444	US-09-925-301-333	Sequence 333, Ap
18	296	90.0	1464	US-10-221-265-686	Sequence 666, Ap
19	296	90.0	1721	US-10-291-172-93	Sequence 93, Appl
20	296	90.0	1721	US-10-221-278-93	Sequence 28, Appl
21	296	90.0	1781	US-10-119-926-48	Sequence 7, Appl
22	281	85.4	512	US-09-918-995-30403	Sequence 30403, A
23	277	84.2	466	US-09-918-995-31769	Sequence 31769, A
24	269	81.8	435	US-09-960-352-4435	Sequence 4435, Ap
25	261	79.3	120239	US-10-332-281-271	Sequence 271, Ap
26	258	78.4	698	US-10-404-460-16	Sequence 16, Appl
27	230	69.9	393	US-09-960-352-5187	Sequence 5187, Ap
28	225	68.4	241	US-09-960-352-9174	Sequence 9174, Ap
29	205	62.3	353	US-09-960-352-15044	Sequence 15044, A
30	182	55.3	1731	US-10-369-738-6	Sequence 6, Appl
31	182	55.3	1923	US-10-369-738-4	Sequence 4, Appl
32	182	55.3	2948	US-10-007-880A-129	Sequence 129, App
33	182	55.3	3063	US-10-007-880A-130	Sequence 130, App
34	182	55.3	3301	US-09-794-589-1	Sequence 1, Appl
35	182	55.3	3301	US-10-315-380-1	Sequence 1, Appl
36	176	53.5	1716	US-10-369-738-1	Sequence 1, Appl
37	176	53.5	1716	US-10-369-738-48	Sequence 2, Appl
38	176	53.5	1716	US-10-369-738-48	Sequence 48, Appl
39	173	52.6	202	US-10-361-997-50	Sequence 50, Appl
40	173	52.6	207	US-10-361-997-49	Sequence 49, Appl
41	173	52.6	1977	US-10-361-997-51	Sequence 51, Appl
42	173	52.6	1977	US-10-361-997-53	Sequence 53, Appl
43	172	52.3	1476	US-10-021-963-1	Sequence 1, Appl
44	172	52.3	1476	US-10-029-386-24789	Sequence 24789, A
45	172	52.3	1647	US-10-239-663-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-361-997-57
Sequence 57, Application US/10361997
Publication No. US20040171794A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
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SEQ ID NO 57
LENGTH: 190
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: DNA sequence of the C-Terminal BamHI-HindIII
OTHER INFORMATION: DX-890 cDNA
US-10-361-997-57

Alignment Scores:

Pred. No.: 6, 72e-41 Length: 190
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-57 (1-190)

QY 1 GIUAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 13 GAAGCTGTAAGCTTGGCAATGTTAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 72
QY 21 PheAspAlaValIleGlyGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 73 TTCGATGCTTAAGGTAAGTGTGTTTGTCCCATATGATGATGTTGTCAAGGTAAAGCT 132
QY 41 AsnIlePheTyrSerGluIleGlyGluCysArgGlyTyrCysGlyValPro 56
DB 133 AACAAATTCTACTGTAAGAAAGATGATGAGAAATCTGTGGTGTCCA 180

RESULT 2

US-10-361-997-56
Sequence 56, Application US/10361997
Publication No. US2004017194A1

GENERAL INFORMATION:

APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 195
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA sequence of the N-Terminal BglII-BamHI DX-890
OTHER INFORMATION: cDNA
US-10-361-997-56

Alignment Scores:

Pred. No.: 6, 94e-41 Length: 195
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-56 (1-195)

QY 1 GIUAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 19 GAAGCTGTAAGCTTGGCAATGTTAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 78
QY 21 PheAspAlaValIleGlyGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 79 TTCGATGCTTAAGGTAAGTGTGTTTGTCCCATATGATGATGTTGTCAAGGTAAAGCT 138
QY 41 AsnIlePheTyrSerGluIleGlyGluCysArgGlyTyrCysGlyValPro 56
DB 139 AACAAATTCTACTGTAAGAAAGATGATGAGAAATCTGTGGTGTCCA 186

RESULT 3

US-10-361-997-72
Sequence 72, Application US/10361997
Publication No. US2004017194A1
GENERAL INFORMATION:

APPLICANT: Ladner, Robert Charles
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
FILE REFERENCE: 3421.1015-000
CURRENT APPLICATION NUMBER: US/10/361,997
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 60/355,547
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 207
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA to insert at BspEI/KpnI site for 2nd encoding
OTHER INFORMATION: of DX-890
US-10-361-997-72

Alignment Scores:

Pred. No.: 7, 47e-41 Length: 207
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-72 (1-207)

QY 1 GIUAlaCyAsnLeuProIleValArgGlyProCySileAlaPhePheProArgTrpAla 20
DB 28 GAAGCTGTAAGCTTGGCAATGTTAGAGGTCCATGATGCTTCTTCCCAAGATGGGCT 87
QY 21 PheAspAlaValIleGlyGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 88 TTGACGCGCTCAAGCAAGCAATGCTCTTTTCTTACGCGGTTGCAAGGCAATGCT 147
QY 41 AsnIlePheTyrSerGluIleGlyGluCysArgGlyTyrCysGlyValPro 56
DB 148 AATAAATTCTACTGTAAGAAAGATGATGAGAAATCTGTGGTGTCCA 195

RESULT 4

US-10-038-722-73
Sequence 73, Application US/10038722
Publication No. US20030175919A1
GENERAL INFORMATION:

APPLICANT: Ley, Arthur C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
FILE REFERENCE: LEY-18
CURRENT APPLICATION NUMBER: US/10/038,722
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 08/849,406
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/US95/16349
PRIOR FILING DATE: 1995-12-15
PRIOR APPLICATION NUMBER: US 08/358,160
PRIOR FILING DATE: 1994-12-16
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73
LENGTH: 444
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

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; OTHER INFORMATION: BstBI-AatII-EcoRI cassette for expression of Epi-HNE-4 (Table 252)
; OTHER INFORMATION: )
US-10-038-722-73

Alignment Scores:
Pred. No.: 1,93e-40 Length: 444
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-038-722-27 (1-56) x US-10-038-722-73 (1-444)

QY 1 GIUAIACyAsnLeuProIleValArgGlyProCySIIeAlaPhePheProArgTPa 20
DB 265 GAGGCTGTGAAGCTTGCATTCGACAGGTCATGATTCCTTCCCAAGATGGGCT 324
QY 21 PheAspAlaValIleGlySIVaIleuPheProTyrGlyGlyCySgInglyAnngly 40
DB 325 TTCGACGCTGTAAAGGTAAAGTGGCTTGTTCCTTCCATAGGCTGTGTCAAGGTAAAGGT 384
QY 41 AenlyPheTyrSerGlyIleGlySIVaIleuPheProTyrGlyGlyValPro 56
DB 385 AACAACTTCTACTGTGAAGAGAGGTAGAGACTGTGTGTCCA 432

RESULT 5
US-10-361-997-58
; Sequence 58, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of the N-Terminal
; OTHER INFORMATION: DX-890-(GGG)4GG-albumin fusion coding region
US-10-361-997-58

Alignment Scores:
Pred. No.: 1,23e-39 Length: 1965
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-58 (1-1965)

QY 1 GIUAIACyAsnLeuProIleValArgGlyProCySIIeAlaPhePheProArgTPa 20
DB 1 GAGGCTGTGAAGCTTGCATTCGACAGGTCATGATTCCTTCCCAAGATGGGCT 60
QY 21 PheAspAlaValIleGlySIVaIleuPheProTyrGlyGlyCySgInglyAnngly 40
DB 61 TTCGATGCTGTAAAGGTAAAGTGGCTTGTTCCTTCCATAGGCTGTGTCAAGGTAAAGGT 120
QY 41 AenlyPheTyrSerGlyIleGlySIVaIleuPheProTyrGlyGlyValPro 56
DB 121 AACAACTTCTACTGTGAAGAGAGGTAGAGACTGTGTGTCCA 168

RESULT 6
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US-10-361-997-60
; Sequence 60, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of the C-Terminal
; OTHER INFORMATION: albumin-(GGG)4GG-DX-890 fusion coding region
US-10-361-997-60

Alignment Scores:
Pred. No.: 1,23e-39 Length: 1965
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-60 (1-1965)

QY 1 GIUAIACyAsnLeuProIleValArgGlyProCySIIeAlaPhePheProArgTPa 20
DB 1798 GAGGCTGTGAAGCTTGCATTCGACAGGTCATGATTCCTTCCCAAGATGGGCT 1857
QY 21 PheAspAlaValIleGlySIVaIleuPheProTyrGlyGlyCySgInglyAnngly 40
DB 1858 TTCGATGCTGTAAAGGTAAAGTGGCTTGTTCCTTCCATAGGCTGTGTCAAGGTAAAGGT 1917
QY 41 AenlyPheTyrSerGlyIleGlySIVaIleuPheProTyrGlyGlyValPro 56
DB 1918 AACAACTTCTACTGTGAAGAGAGGTAGAGACTGTGTGTCCA 1965

RESULT 7
US-10-361-997-70
; Sequence 70, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 3255
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NotI cassette of pDB2300X2 with DX890 (Nterm) and
; OTHER INFORMATION: Cterm linker ready for second DX890
US-10-361-997-70

Alignment Scores:
Pred. No.: 2,3e-39 Length: 3255
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 18      Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-70 (1-3255)

QY 1 GUAACyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTTPala 20
DB 901 GAAGCGTGAATTCGCAATGTTAGAGGTCATGATGCTTCTCCCAAGATGGGCT 960
QY 21 PheAspAlaValIleGlyCysValIleuPheProTyrGlyCysGlnGlyAsnGly 40
DB 961 TTCGATGCTGTTAAGGTAAGTGTGTTGTTCCCATATGAGGTGTCTCAAGGTACGGT 1020

QY 41 AsnLysPheTyrSerGlnLysGluCysArgGlyTyrCysGlyValPro 56
DB 1021 AACAGTCTTACTCTGAAAAGAGATGTAGGAATATCTGTGGTTCCTCA 1068

RESULT 9
US-10-361-997-44
; Sequence 44, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000

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; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 3444
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DPL-14-(GGS)4 GG-RHA-(GGS)4-GG-DX-890 DNA sequence
US-10-361-997-44

Alignment Scores:
Pred. No.: 2,466-39      Length: 3444
Score: 329.00      Matches: 56
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 18      Gaps: 0

US-10-038-722-27 (1-56) x US-10-361-997-44 (1-3444)

QY 1 GUAACyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTTPala 20
DB 2920 GAGGCTTCAATCTTCATGCTGCGCCCTTGCAATGCGCTTTTCTTCGTTGGGCGC 2979
QY 21 PheAspAlaValIleGlyCysValIleuPheProTyrGlyCysGlnGlyAsnGly 40
DB 2980 TTGACGCGCTCAAGGCAATGCGCTTTTCTTCAGCGGTTGCCAGGCAATGCGC 3039

QY 41 AsnLysPheTyrSerGlnLysGluCysArgGlyTyrCysGlyValPro 56
DB 3040 AATAATTATTATAGCGAAGAGAGTCCGCTAGATATCGGCGCTCCCT 3087

RESULT 10
US-10-038-722-71
; Sequence 71, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS NHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 8584
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid PHIL-D2 (MraI)pharePro::EPI-HNE-3) (Table 251)
US-10-038-722-71

Alignment Scores:
Pred. No.: 4,446-38      Length: 8584
Score: 324.00      Matches: 55
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 98.48%      Indels: 0

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DB: 16 Gaps: 0

US-10-038-722-27 (1-56) x US-10-038-722-71 (1-8584)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
1212 GCTTGTAATTCATCCATCGTCAGAGTCATGCTTCTTCCCAAGATGGGCTTTC 1271

QY 22 AspaIValIySGIlyLysCysValIeuPheProTyrgIyGlyCysGlnGlyAsnGlyAsn 41
1272 GACGCTGTAAAGGGAAGGAGGCTGTGTTCCCAACGGGAGGAGTGTACAGGTAAAC 1331

QY 42 LysPheTySerGluLysGluCysArgGluTyrgCysGlyValPro 56
1332 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGCTTCCA 1376

DB 1332 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGCTTCCA 1376

RESULT 11

US-10-038-722-75

/ Sequence 75, Application US/10038722
/ Publication No. US20030175919A1

/ GENERAL INFORMATION:
/ APPLICANT: LEY, Arthur C.
/ APPLICANT: GUTERMAN, Sonia K.
/ APPLICANT: MARKLAND, William
/ APPLICANT: KENT, Rachel B.
/ APPLICANT: ROBERTS, Bruce L.
/ APPLICANT: LADNER, Robert C.
/ TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
/ FILE REFERENCE: LEY-1B
/ CURRENT APPLICATION NUMBER: US/10/038,722
/ CURRENT FILING DATE: 2002-01-08
/ PRIOR APPLICATION NUMBER: US 08/849,406
/ PRIOR FILING DATE: 1999-07-21
/ PRIOR APPLICATION NUMBER: PCT/US95/16349
/ PRIOR FILING DATE: 1995-12-15
/ PRIOR APPLICATION NUMBER: US 08/358,160
/ PRIOR FILING DATE: 1994-12-16
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 75
/ LENGTH: 8590
/ TYPE: DNA
/ ORGANISM: Artificial Sequence

/ OTHER INFORMATION: p02pick (MFAlphaprepro::EPI-NHE-3) circular dedNA (Table 253)

US-10-038-722-75

Alignment Scores:

Pred. No.:	4,45e-38	Length:	8590
Score:	324.00	Matches:	55
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.48%	Indels:	0
DB:	16	Gaps:	0

US-10-038-722-27 (1-56) x US-10-038-722-75 (1-8590)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
1212 GCTTGTAATTCATCCATCGTCAGAGTCATGCTTCTTCCCAAGATGGGCTTTC 1271

QY 22 AspaIValIySGIlyLysCysValIeuPheProTyrgIyGlyCysGlnGlyAsnGlyAsn 41
1272 GACGCTGTAAAGGGAAGGAGGCTGTGTTCCCAACGGGAGGAGTGTACAGGTAAAC 1331

QY 42 LysPheTySerGluLysGluCysArgGluTyrgCysGlyValPro 56
1332 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGCTTCCA 1376

DB 1332 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGCTTCCA 1376

RESULT 12

US-10-298-796-27

/ Sequence 27, Application US/10298796
/ Publication No. US20030220490A1

/ GENERAL INFORMATION:
/ APPLICANT: KURIYAMA, Shinichi
/ APPLICANT: HASEGAWA, Takashi
/ TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
/ FILE REFERENCE: 1110-253P
/ CURRENT APPLICATION NUMBER: US/10/298,796
/ CURRENT FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: US/09/331,793
/ PRIOR FILING DATE: 1999-06-25
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 27
/ LENGTH: 204
/ TYPE: DNA
/ ORGANISM: Homo Sapiens

US-10-298-796-27

Alignment Scores:

Pred. No.:	8.01e-36	Length:	204
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	17	Gaps:	0

US-10-038-722-27 (1-56) x US-10-298-796-27 (1-204)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
4 GCTTGCAATCTCCCATGTCGCGGCGCCCTGCGAGCTTCATCCAGCTCGGCATTT 63

QY 22 AspaIValIySGIlyLysCysValIeuPheProTyrgIyGlyCysGlnGlyAsnGlyAsn 41
64 GATGCTGTCAAGGGAAGTGGCTCTTCCCTTACGGAGGCTGCCAGGCAACGGGAAAC 123

QY 42 LysPheTySerGluLysGluCysArgGluTyrgCysGlyValPro 56
124 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGCTTCCCT 168

DB 124 AAGTCTACTCTGAGAGAGAGTGTAGAGTACTGTGCTTCCCT 168

RESULT 13

US-09-918-995-8710

/ Sequence 8710, Application US/09918995
/ Publication No. US20030073623A1

/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918,995
/ CURRENT FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8710
/ LENGTH: 408
/ TYPE: DNA
/ ORGANISM: Homo sapiens

US-09-918-995-8710

Alignment Scores:

Pred. No.:	1.9e-35	Length:	408
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	10	Gaps:	0

US-10-038-722-27 (1-56) x US-09-918-995-8710 (1-408)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
218 GCTTGCAATCTCCCATGTCGCGGCGCCCTGCGAGCTTCATCCAGCTCGGCATTT 277

```
Qy 22 AspaIaValIySGIyLysCyseValIleuPheProTyrgIyGIyCyseGInGIyAsnGIyAsn 41
Db 278 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTACGGGGGGCTGCCAGGGCAACGGGAAC 337
Qy 42 LysPheTySerGIuLysGIuCyseArgGIuTyrcySGIyValPro 56
Db 338 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCCT 382

RESULT 14
US-10-298-796-28
; Sequence 28, Application US/10298796
; Publication No. US20030220490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-298-796-28

Alignment Scores:
Pred. No.: 2,09e-35 Length: 441
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservatve: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 17 Gaps: 0

US-10-038-722-27 (1-56) x US-10-298-796-28 (1-441)

Qy 2 AlaCyseAeuLeuProIleValIArgGIyProCyseIleAlaPhePheProArgTTPAlaPhe 21
Db 241 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATTT 300
Qy 22 AspaIaValIySGIyLysCyseValIleuPheProTyrgIyGIyCyseGInGIyAsnGIyAsn 41
Db 301 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTACGGGGGGCTGCCAGGGCAACGGGAAC 360
Qy 42 LysPheTySerGIuLysGIuCyseArgGIuTyrcySGIyValPro 56
Db 361 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCCT 405

RESULT 15
US-10-291-265-214
; Sequence 214, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 214
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (103)..(1158)
US-10-291-265-214

Alignment Scores:
Pred. No.: 7.85e-35 Length: 1280
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservatve: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 17 Gaps: 0

US-10-038-722-27 (1-56) x US-10-291-265-214 (1-1280)

Qy 2 AlaCyseAeuLeuProIleValIArgGIyProCyseIleAlaPhePheProArgTTPAlaPhe 21
Db 958 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGGCATTT 1017
Qy 22 AspaIaValIySGIyLysCyseValIleuPheProTyrgIyGIyCyseGInGIyAsnGIyAsn 41
Db 1018 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTACGGGGGGCTGCCAGGGCAACGGGAAC 1077
Qy 42 LysPheTySerGIuLysGIuCyseArgGIuTyrcySGIyValPro 56
Db 1078 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCCT 1122
```

```
RESULT 16
US-09-978-418-7
; Sequence 7, Application US/09978418
; Publication No. US2003011897A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephan
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 142.US5.REG
; CURRENT APPLICATION NUMBER: US/09/978,418
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/311,305
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/314,734
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/318,204
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/326,470
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..263
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 264..926
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 927..1436
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1404..1409
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 1421..1436
US-09-978-418-7
```

Alignment Scores: 9.06e-35 Length: 1436
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 10 Gaps: 0
DB: 10

US-10-038-722-27 (1-56) x US-09-925-301-333 (1-1436)

QY 2 AlaCysAsnLeuProIleValArgIlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 1117 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATT 1176

QY 22 AspaIaValIySGIlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 1177 GATGCTGTCAAGGGAGAGTGCCTCTCCCTACGGGGGCTGCACAGGCAACGGGAAC 1236

QY 42 LysPheTyrSerGlyLysGlyLysCysArgIlyTyrCysGlyValPro 56
DB 1237 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTCTCCT 1281

RESULT 17
US-09-925-301-333
Sequence 333, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 333
LENGTH: 1444
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-301-333

Alignment Scores: 9.12e-35 Length: 1444
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 9 Gaps: 0
DB: 9

US-10-038-722-27 (1-56) x US-09-925-301-333 (1-1444)

QY 2 AlaCysAsnLeuProIleValArgIlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 1090 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATT 1149

QY 22 AspaIaValIySGIlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 1150 GATGCTGTCAAGGGAGAGTGCCTCTCCCTACGGGGGCTGCACAGGCAACGGGAAC 1209

QY 42 LysPheTyrSerGlyLysGlyLysCysArgIlyTyrCysGlyValPro 56
DB 1210 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTCTCCT 1254

RESULT 18
US-10-291-265-686
Sequence 686, Application US/10291265
Patent No. US20030232054A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al

TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 686
LENGTH: 1464
TYPE: DNA
ORGANISM: Homo sapiens
US-10-291-265-686

Alignment Scores: 9.28e-35 Length: 1464
Pred. No.: 296.00 Matches: 51
Score: 92.73% Conservative: 0
Percent Similarity: 92.73% Mismatches: 4
Best Local Similarity: 89.97% Indels: 0
Query Match: 17 Gaps: 0
DB: 17

US-10-038-722-27 (1-56) x US-10-291-265-686 (1-1464)

QY 2 AlaCysAsnLeuProIleValArgIlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 1143 GCCTCAATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTCGGCATT 1202

QY 22 AspaIaValIySGIlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 1203 GATGCTGTCAAGGGAGAGTGCCTCTCCCTACGGGGGCTGCACAGGCAACGGGAAC 1262

QY 42 LysPheTyrSerGlyLysGlyLysCysArgIlyTyrCysGlyValPro 56
DB 1263 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTCTCCT 1307

RESULT 19
US-10-291-172-93
Sequence 93, Application US/10291172
Patent No. US20030228584A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO: 93
LENGTH: 1721
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (284)..(1339)
FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(1721)
OTHER INFORMATION: n = a,t,c or g
US-10-291-172-93

Alignment Scores:

Pred. No.:	1,13e-34	Length:	1721
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	17	Gaps:	0

US-10-038-722-27 (1-56) x US-10-291-172-93 (1-1721)

QY 2 AlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTyrAlaPhe 21

DB 1139 GCCTGCATCTCCCATATGTCGGGGCCCTGCGAGCCTTCATCCAGCTCTGGGCATTT 1198

QY 22 AspAlaValIleGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

DB 1199 GATGCTGTCAAGGGAGATGGCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 1258

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

DB 1259 AAGTCTACTCAGAGAGAGAGTGCAGAGTACTGCGGTCTCCT 1303

RESULT 20

US-10-221-278-93
Sequence 93, Application US/10221278
Publication No. US20040034208A1

GENERAL INFORMATION:

APPLICANT: HySeq, Inc
TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-045
CURRENT FILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: 09/593,267
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17

PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 752
SEQ ID NO 93

LENGTH: 1721

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (284)...(1339)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(1721)

OTHER INFORMATION: n = a,t,c or g

US-10-221-278-93

Alignment Scores:

Pred. No.:	1,13e-34	Length:	1721
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	17	Gaps:	0

US-10-038-722-27 (1-56) x US-10-221-278-93 (1-1721)

QY 2 AlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTyrAlaPhe 21

DB 1139 GCCTGCATCTCCCATATGTCGGGGCCCTGCGAGCCTTCATCCAGCTCTGGGCATTT 1198

QY 22 AspAlaValIleGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

DB 1199 GATGCTGTCAAGGGAGATGGCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 1258

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

DB 1259 AAGTCTACTCAGAGAGAGATGCAGAGTACTGCGGTCTCCT 1303

RESULT 21

US-10-119-926-48
Sequence 48, Application US/10119926
Publication No. US20030104413A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Zhao, Qing A.

APPLICANT: Chen, Rui-hong

APPLICANT: Wehrman, Tom

APPLICANT: Zhou, Ping

APPLICANT: Xu, Chongjun

APPLICANT: Yang, Yonghong

APPLICANT: Xue, Aidong J.

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20030104413A1el Nucleic Acids and

FILE REFERENCE: 789CIP2B00N

CURRENT APPLICATION NUMBER: US/10/119,926

PRIOR APPLICATION NUMBER: 09/574,454

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/519,705

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 108

SOFTWARE: PC_Fl_genes Version 1.0

SEQ ID NO 48

LENGTH: 1781

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (344)...(1402)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(1781)

OTHER INFORMATION: n = a,t,c or g

US-10-119-926-48

US-10-038-722-27 (1-56) x US-10-119-926-48 (1-1781)

Alignment Scores:

Pred. No.:	1,18e-34	Length:	1781
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	15	Gaps:	0

US-10-038-722-27 (1-56) x US-10-119-926-48 (1-1781)

QY 2 AlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTyrAlaPhe 21

DB 1199 GCCTGCATCTCCCATATGTCGGGGCCCTGCGAGCCTTCATCCAGCTCTGGGCATTT 1258

QY 22 AspAlaValIleGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

DB 1259 GATGCTGTCAAGGGAGATGGCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 1318

QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56

Db 1319 AAGTCTACTCAGAGAGAGTGCGAGTACTGCGGTCCCT 1363

RESULT 22

US-09-918-995-30403

Sequence 30403, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: HySeq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 30403

LENGTH: 512

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(512)

OTHER INFORMATION: n = A,T,C or G

US-09-918-995-30403

Alignment Scores:

Pred. No.: 4,9e-33 Length: 512

Score: 281.00 Matches: 49

Percent Similarity: 89.09% Conservative: 0

Best Local Similarity: 89.09% Mismatches: 6

Query Match: 85.41% Indels: 0

DB: 10 Gaps: 0

US-10-038-722-27 (1-56) x US-09-918-995-30403 (1-512)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21

Db 329 GCTTCATCTCCCATATGTCGGGGGCCCTCCGAGCTTATCCAGCTTGCGCATTT 388

QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

Db 389 GATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 448

QY 42 LysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56

Db 449 AAGTCTACTCAGAGAGAGTGCGAGTACTGCGGTCCCT 493

RESULT 23

US-09-918-995-31769

Sequence 31769, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: HySeq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31769

LENGTH: 466

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(466)

OTHER INFORMATION: n = A,T,C or G

US-09-918-995-31769

Alignment Scores:

Pred. No.: 1,78e-32 Length: 466

Score: 277.00 Matches: 49

Percent Similarity: 89.09% Conservative: 0

Best Local Similarity: 89.09% Mismatches: 6

Query Match: 84.19% Indels: 0

DB: 10 Gaps: 0

US-10-038-722-27 (1-56) x US-09-918-995-31769 (1-466)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21

Db 229 GCTTCATCTCCCATATGTCGGGGGCCCTCCGAGCTTATCCAGCTTGCGCATTT 288

QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41

Db 289 GATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 348

QY 42 LysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56

Db 349 AAGTCTACTCAGAGAGAGTGCGAGTACTGCGGTCCCT 393

RESULT 24

US-09-960-352-4435

Sequence 4435, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengping

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 4435

LENGTH: 435

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 19-LIB34-040-Q1-E1-E3

US-09-960-352-4435

Alignment Scores:

Pred. No.: 2,72e-31 Length: 435

Score: 269.00 Matches: 44

Percent Similarity: 89.29% Conservative: 6

Best Local Similarity: 78.57% Mismatches: 6

Query Match: 81.76% Indels: 0

DB: 9 Gaps: 0

US-10-038-722-27 (1-56) x US-09-960-352-4435 (1-435)

QY 1 GluAlaCysAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAla 20

Db 136 GAGGCTTATCTCCCATATGTCGGGGGCCCTCCGAGCTTATCCAGCTTGCGCA 195

QY 21 PheAspaIaValIyGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGly 40

Db 196 TTTGATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAATGCT 255

QY 41 AsnLysPheTyrSerGluLysGluCysArgGlyTyrCysGlyValPro 56

Db 256 AACAAATTTTACTCGAGAGAGAGTGAAGAGTACTGCGCATTCCT 303

RESULT 25

US-10-322-281-271/C

Sequence 271, Application US/10322281

Publication No. US20040126762A1

GENERAL INFORMATION:

```

1  APPLICANT: David W. Morris
2  APPLICANT: Marc S. Malandro
3  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
4  FILE REFERENCE: 52945201000
5  CURRENT APPLICATION NUMBER: US/10/322,281
6  CURRENT FILING DATE: 2002-12-17
7  NUMBER OF SEQ ID NOS: 866
8  SOFTWARE: FastSeq for Windows Version 4.0
9  SEQ ID NO: 271
10 LENGTH: 120239
11
12 TYPE: DNA
13
14 ORGANISM: Mus musculus
15
16 FEATURE:
17 NAME/KEY: misc_feature
18 LOCATION: (1)..(120239)
19
20 OTHER INFORMATION: n = A,T,C or G
21
22 US-10-322-281-271

```

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:35:51 ; Search time 2303 Seconds
(without alignments)
925.575 Million cell updates/sec

Title: US-10-038-722-27
Perfect score: 329
Sequence: 1 EACNLPYVRGPCIAPFFPRMA.....QGNNGKFXSEKREYCVGP 56

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+g2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US10038722/runat_18022005_145235_14331/app_query.fasta.1.199
-DB=EST -QFMT=fastap -SUPFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT2=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10038722@cgn 1.1.4352@runat_18022005_145235_14331 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DISPATCH=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	296	90.0	383	1	AV696152
2	296	90.0	387	1	AV686452
3	296	90.0	394	1	AV657651
4	296	90.0	417	1	AV656508
5	296	90.0	417	1	AV695187
6	296	90.0	449	1	AV682129
7	296	90.0	450	1	AI114613
8	296	90.0	487	1	AI246161
9	296	90.0	520	1	AV720273

c	10	296	90.0	525	1	AI333042	AI333042	qq31h04.x
c	11	296	90.0	535	1	AV654685	AV654685	AV654685
c	12	296	90.0	543	6	CB144250	K-EST0198	CB144250
c	13	296	90.0	543	6	CB148803	K-EST0205	CB148803
c	14	296	90.0	550	1	AI193912	ge73b01.x	AI193912
c	15	296	90.0	571	1	AI207590	HA2954.Hu	AI207590
c	16	296	90.0	583	1	AI336247	qt45b07.x	AI336247
c	17	296	90.0	617	1	AV683002	AV683002	AV683002
c	18	296	90.0	644	1	AI807643	wf49d04.x	AI807643
c	19	296	90.0	670	1	AV686492	AV686492	AV686492
c	20	296	90.0	675	2	AM173259	xj85c08.x	AM173259
c	21	296	90.0	682	1	AV686493	AV686493	AV686493
c	22	296	90.0	683	1	AV645324	AV645324	AV645324
c	23	296	90.0	687	1	AV700236	AV700236	AV700236
c	24	296	90.0	692	1	AV645372	AV645372	AV645372
c	25	296	90.0	692	5	BU689265	UI-CF-EC1	BU689265
c	26	296	90.0	704	1	AV682021	AV682021	AV682021
c	27	296	90.0	751	1	AV700675	AV700675	AV700675
c	28	296	90.0	825	1	AI191043	qe25a09.x	AI191043
c	29	296	90.0	826	1	AI375135	lc09g08.x	AI375135
c	30	296	90.0	877	5	BK405852	BK405852	BK405852
c	31	296	90.0	879	3	CR616173	full-1eng	CR616173
c	32	296	90.0	970	5	BO653816	AGENCOURT	BO653816
c	33	296	90.0	1155	3	CR607981	full-1eng	CR607981
c	34	296	90.0	1268	3	CR615737	full-1eng	CR615737
c	35	295	89.7	509	5	BO650357	AGENCOURT	BO650357
c	36	292	88.8	507	6	CB147193	K-EST0202	CB147193
c	37	289	87.8	626	1	AV658823	AV658823	AV658823
c	38	288	87.5	439	7	CR763328	DKF2p4701	CR763328
c	39	288	87.5	471	7	CR763216	DKF2p470M	CR763216
c	40	288	87.5	557	7	CR773258	DKF2p470E	CR773258
c	41	288	87.5	704	7	CO774863	ILLUMIGEN	CO774863
c	42	288	87.5	787	7	CO775068	ILLUMIGEN	CO775068
c	43	288	87.5	931	7	CO774307	ILLUMIGEN	CO774307
c	44	286	86.9	660	1	AV699605	AV699605	AV699605
c	45	285	86.6	613	6	CA866791	1t7f102.x	CA866791

ALIGNMENTS

RESULT 1
LOCUS: AV696152 383 bp mRNA linear EST 16-JAN-2002
DEFINITION: AV696152 GKC Homo sapiens cDNA clone GKCBCP06 5', mRNA sequence.
ACCESSION: AV696152
VERSION: AV696152.1 GI:10298015
KEYWORDS: EST.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens

REFERENCE
AUTHORS: Xiao,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,X., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE: Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL: Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE: 21625106
PUBMED: 11752456

COMMENT: Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..383
/organism="Homo sapiens"

FEATURES
source

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCBPG06"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1ib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ALIGNMENT SCORES:

Alignment Scores:

Pred. No.:	2,23e-28	Length:	383
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x AV696152 (1-383)

QY 2 AAlaCysAenLeuProIleValArgIyProCysIleAlaPhePheProArgTrpAlaPhe 21
|||||
DB 56 GCTGCAATCTCCCATAGTCCGGGGCCCTCCGCCAGACCTTCATCCAGCTCGGGCATT 115
|||||
QY 22 AaPaIaValIyGlyLyCySValIeupheProTyrgIyGlyCySgInglyAanGlyAan 41
|||||
DB 116 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 175
|||||
QY 42 LysPheTySerGluIyGluCyAArgIyTyrgIyGlyValPro 56
|||||
DB 176 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 220
|||||

RESULT 2

LOCUS AV686452 387 bp mRNA linear EST 16-JAN-2002
DEFINITION AV686452 GKC Homo sapiens cDNA clone GKAEF08 5', mRNA sequence.
ACCESSION AV686452
VERSION AV686452.1 GI:10288315

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 387)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Pu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

TITLE

JOURNAL MEDLINE PUBLISHED
COMMENT Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source 1..387
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKAEF08"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1ib="GKC"

ORIGIN

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ALIGNMENT SCORES:

Pred. No.:	2,26e-28	Length:	387
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x AV686452 (1-387)

QY 2 AAlaCysAenLeuProIleValArgIyProCysIleAlaPhePheProArgTrpAlaPhe 21
|||||
DB 57 GCTGCAATCTCCCATAGTCCGGGGCCCTCCGCCAGACCTTCATCCAGCTCGGGCATT 116
|||||
QY 22 AaPaIaValIyGlyLyCySValIeupheProTyrgIyGlyCySgInglyAanGlyAan 41
|||||
DB 117 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 176
|||||
QY 42 LysPheTySerGluIyGluCyAArgIyTyrgIyGlyValPro 56
|||||
DB 177 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCT 221
|||||

RESULT 3

LOCUS AV657651 394 bp mRNA linear EST 16-JAN-2002
DEFINITION AV657651 GLC Homo sapiens cDNA clone GLCFB05 3', mRNA sequence.
ACCESSION AV657651
VERSION AV657651.1 GI:9878665

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 394)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Pu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

TITLE

JOURNAL MEDLINE PUBLISHED
COMMENT Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source 1..394
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCFB05"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1ib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	2,31e-28	Length:	394
Score:	296.00 <td>Matches:</td> <td>51 </td>	Matches:	51

Percent Similarity: 92.73%
 Best Local Similarity: 92.73%
 Query Match: 89.97%
 DB: 1
 Gaps: 0

US-10-038-722-27 (1-56) x AV657651 (1-394)

QY 2 AlaCysaenLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
 DB 67 GCTGCATCTCTCCCATAGTCCGGGGCCCCCTCCGAGCTTCATCCAGCTCGGCATT 126
 QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrglyGlyCysGlnGlyAsnGlyAsn 41
 DB 127 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCCAGGGCAACGGAAAC 186
 QY 42 LysPheTyrsenGluLysGluCysArgGlyLutyrCysGlyValPro 56
 DB 187 AAGTCTACTCAGAGAGAGTGCAGAGATGCTGCGGTCTCT 231

RESULT 4
 LOCUS AV656508 417 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV656508 GLC Homo sapiens cDNA clone GLCESA11 3', mRNA sequence.
 ACCESSION AV656508
 VERSION AV656508.1 GI:9877522
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 417)
 AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z., and Han,Z.
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 MEDLINE 21625106
 PUBMED 11752456

COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 source
 1..417
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GLCESA11"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="GCR"
 /clone_lib="GCR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI, Site_2: XhoI"

ORIGIN

Alignment Scores:
 Pred. No.: 2.48e-28 Length: 417
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservatve: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV656508 (1-417)

QY 2 AlaCysaenLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
 DB 88 GCTGCATCTCTCCCATAGTCCGGGGCCCCCTCCGAGCTTCATCCAGCTCGGCATT 147
 QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrglyGlyCysGlnGlyAsnGlyAsn 41
 DB 148 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCCAGGGCAACGGAAAC 207
 QY 42 LysPheTyrsenGluLysGluCysArgGlyLutyrCysGlyValPro 56
 DB 208 AAGTCTACTCAGAGAGAGTGCAGAGATGCTGCGGTCTCT 252

RESULT 5
 LOCUS AV695187 417 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV695187 GKC Homo sapiens cDNA clone GKCBM01 5', mRNA sequence.
 ACCESSION AV695187
 VERSION AV695187.1 GI:10297050
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 417)
 AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z., and Han,Z.
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 MEDLINE 21625106
 PUBMED 11752456
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 source
 1..417
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKCBM01"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="GCR"
 /clone_lib="GCR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI, Site_2: XhoI"

ORIGIN

Alignment Scores:
 Pred. No.: 2.48e-28 Length: 417
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservatve: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV695187 (1-417)

QY 2 AlaCysaenLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
 DB 95 GCTGCATCTCTCCCATAGTCCGGGGCCCCCTCCGAGCTTCATCCAGCTCGGCATT 154
 QY 22 AspaIaValIyGlyLysCysValIleuPheProTyrglyGlyCysGlnGlyAsnGlyAsn 41
 DB 155 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTACGGGGGCTGCCAGGGCAACGGAAAC 214

QY 42 LysPheTYrSerGluTyGluCySArgGluTYrCYSGlyValPro 56
 DB 215 AAGTCTACTCAGAGAAGAGTCCAGAGTACTCGGCTGTCCT 259
 RESULT 6
 LOCUS AV682129 449 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV682129 GKB Homo sapiens cDNA clone GKBAB06 5', mRNA sequence.
 ACCESSION AV682129
 VERSION AV682129.1 GI:10283992
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 449)
 Xue, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Pu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z. and Han, Z.
 Hu, G., Gu, J., Chen, Z. and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 JOURNAL 11752456
 MEDLINE 21625106
 PUBMED 11752456
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 FEATURES
 source
 1..449
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKBAB06"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_1ib="GKB"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,72e-28 Length: 449
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0
 US-10-038-722-27 (1-56) x AV682129 (1-449)
 QY 2 A1aCySAsnLeuProIleValAlaGlyProCySileAlaPhePheProArgTTPAlaPhe 21
 DB 122 GCCTGCATCTCCCATAGTCGGGGCCCTGCGAGCCTTATCCAGCTCTGGGCAATT 181
 QY 22 AapAlaValAllyGlyCySValIleuPheProTYrGlyGlyCySgInglyAsnGlyAen 41
 DB 182 GATGCTGTCAAGAGGGAAGTGGCTCTTCCCTTACGAGGGGCTGCCAGGCAACGGGAAC 241
 QY 42 LysPheTYrSerGluTyGluCySArgGluTYrCYSGlyValPro 56
 DB 242 AAGTCTACTCAGAGAAGAGTCCAGAGTACTCGGCTGTCCT 286
 RESULT 7
 A1114613

LOCUS A1114613 450 bp mRNA linear EST 11-NOV-1999
 DEFINITION HA1200 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION A1114613
 VERSION A1114613.1 GI:6359958
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 450)
 Yu, Y., Zhang, C., Luo, L., Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M.
 and He, F.
 Expression profile analysis of a human fetal liver cDNA library
 Unpublished (1998)
 TITLE Unpublished (1998)
 JOURNAL Contact: Yongtao Yu
 Department of Hematology
 Beijing Institute of Radiation Medicine
 27 Taiping Road, Beijing 100850, P.R.China
 Tel: 0086-10-68159479
 Fax: 0086-10-68214653
 Email: yyr48@yahoo.com.
 FEATURES
 source
 1..450
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="liver"
 /dev_stage="fetal"
 /lab_host="WC1061/P3"
 /clone_1ib="Human fetal liver cDNA library"
 /note="Vector: pCDNA1"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,73e-28 Length: 450
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0
 US-10-038-722-27 (1-56) x A1114613 (1-450)
 QY 2 A1aCySAsnLeuProIleValAlaGlyProCySileAlaPhePheProArgTTPAlaPhe 21
 DB 120 GCCTGCATCTCCCATAGTCGGGGCCCTGCGAGCCTTATCCAGCTCTGGGCAATT 179
 QY 22 AapAlaValAllyGlyCySValIleuPheProTYrGlyGlyCySgInglyAsnGlyAen 41
 DB 180 GATGCTGTCAAGAGGGAAGTGGCTCTTCCCTTACGAGGGGCTGCCAGGCAACGGGAAC 239
 QY 42 LysPheTYrSerGluTyGluCySArgGluTYrCYSGlyValPro 56
 DB 240 AAGTCTACTCAGAGAAGAGTCCAGAGTACTCGGCTGTCCT 284
 RESULT 8
 A1246161/c
 LOCUS A1246161 487 bp mRNA linear EST 28-JAN-1999
 DEFINITION q129b06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1857875
 3' similar to gb:X04225 ALPHA-1-MICROGLOBULIN (HUMAN);, mRNA
 sequence.
 ACCESSION A1246161
 VERSION A1246161.1 GI:3841558
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 487)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgsbbs-remail.nih.gov

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 511 Std Error: 0.00
Seq primer: -40UP from Gldco

High quality sequence stop: 331.
Location/Qualifiers

FEATURES
SOURCE

1..487

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1857875"

/tissue_type="Pooled human melanocyte, fetal heart, and

pregnant uterus"

/lab_host="DH10B"

/clone_lib="Soares NHPu S1"

/note="Organ: mixed (see below); Vector: pT7T3D-Pac

(Pharmacia) with a modified polylinker; Site 1: Not 1;

Site 2: Eco RI; Equal amounts of plasmid DNA from three

normalized libraries (melanocyte 2bHM, pregnant uterus

NbHpu, and fetal heart NbH19w) were mixed, and 88 circles

were made in vitro. Following HAP purification, this DNA

was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from pools of

5,000 clones made from the same 3 libraries. The pools

consisted of 1.M.A.G.B. clones 260232-265223,

340488-345479, and 484488-489479."

ORIGIN

Alignment Scores:

Pred. No.: 3,02e-28 Length: 487
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x A1246161 (1-487)

Qy 2 A1aCysAenLeuProIleValaIarGlyProCysIleAlaPheProArgTrpAlaPhe 21

Db 316 GCCTGCATCTCCCATATGTCGGGGCCCGCGAGCCTTCATCCAGCTCGGCATT 257

Qy 22 AspaIaValIySGlyLyvCySvalleuPheProTyrglyGlyCySgInGlyAsnGlyAsn 41

Db 256 GATGCTGTCAAGGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCCAGGGCAACCGGAAC 197

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 196 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 152

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 196 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 152

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 196 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 152

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 196 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 152

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 196 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 152

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 196 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 152

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 196 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 152

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 196 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 152

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers

FEATURES
SOURCE

1..520

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="GLCBA03"

/tissue_type="corresponding non cancerous liver tissue"

/dev_stage="Adult"

/lab_host="SOIR"

/clone_lib="GLC"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:

XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 3.28e-28 Length: 520
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV720273 (1-520)

Qy 2 A1aCysAenLeuProIleValaIarGlyProCysIleAlaPheProArgTrpAlaPhe 21

Db 317 GCCTGCATCTCCCATATGTCGGGGCCCGCGAGCCTTCATCCAGCTCGGCATT 258

Qy 22 AspaIaValIySGlyLyvCySvalleuPheProTyrglyGlyCySgInGlyAsnGlyAsn 41

Db 257 GATGCTGTCAAGGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCCAGGGCAACCGGAAC 198

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers

FEATURES
SOURCE

1..525

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="GLCBA03"

/tissue_type="corresponding non cancerous liver tissue"

/dev_stage="Adult"

/lab_host="SOIR"

/clone_lib="GLC"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:

XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 3.28e-28 Length: 520
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV720273 (1-520)

Qy 2 A1aCysAenLeuProIleValaIarGlyProCysIleAlaPheProArgTrpAlaPhe 21

Db 317 GCCTGCATCTCCCATATGTCGGGGCCCGCGAGCCTTCATCCAGCTCGGCATT 258

Qy 22 AspaIaValIySGlyLyvCySvalleuPheProTyrglyGlyCySgInGlyAsnGlyAsn 41

Db 257 GATGCTGTCAAGGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCCAGGGCAACCGGAAC 198

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

Qy 42 LysPheTySerGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyvGlyv 56

Db 197 AAGTTCATCTCAGAGAGAGTGCAGAGATCTCGGTGTCCT 153

/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soareg_NHMPU_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NBHPU, and fetal heart NBH19M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1 M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Alignment Scores:

Pred. No.:	3.32e-28	Length:	525
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x A1333042 (1-525)

QY 2 A1ACySaAnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21

DB 337 GCCTGCATCTCCCATAGTCGCGGGCCCTCGCGAGCCTTCATCCAGCTTTGGGCAATT 278

QY 22 AspaIaValIyGlyGlyCysValIleuPheProTyGlyGlyCysGlnGlyAsnGlyAsn 41

DB 277 GATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 218

QY 42 LysPheTySerGluIyGlyCysArgGlyIyTyCysGlyValPro 56

DB 217 AAGTTTACTCAGAGAGAGTGCAGAGTACTGCGGTGCCCT 173

RESULT 11

AV654685

LOCUS AV654685 535 bp mRNA linear EST 15-JAN-2002

DEFINITION AV654685 GUC Homo sapiens cDNA clone G1CDYD11 3', mRNA sequence.

ACCESSION AV654685

VERSION AV654685.1 GI:9875699

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 535)

AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,

Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,

Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,

Hu,G., Gu,J., Chen,Z. and Han,Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level

by comparing gene expression profiles of hepatocellular carcinoma

with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE 21625106

COMMENT 11752456

CONTACT: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1..535

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="G1CDYD11"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="adult"
/lab_host="SOAR"
/clone_lib="GUC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	3.4e-28	Length:	535
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x AV654685 (1-535)

QY 2 A1ACySaAnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21

DB 127 GCCTGCATCTCCCATAGTCGCGGGCCCTCGCGAGCCTTCATCCAGCTTTGGGCAATT 186

QY 22 AspaIaValIyGlyGlyCysValIleuPheProTyGlyGlyCysGlnGlyAsnGlyAsn 41

DB 187 GATGCTGTCAAGGGAGAGTGCCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC 246

QY 42 LysPheTySerGluIyGlyCysArgGlyIyTyCysGlyValPro 56

DB 247 AAGTTTACTCAGAGAGAGTGCAGAGTACTGCGGTGCCCT 291

RESULT 12

CB144250

LOCUS CB144250 543 bp mRNA linear EST 29-JAN-2003

DEFINITION K-EST0198507 L7N800102s1 Homo sapiens cDNA clone L7N800102s1-22-F06

ACCESSION CB144250

VERSION CB144250.1 GI:28122110

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 543)

AUTHORS Oh,K.U., Cheong,J.E., Sohn,H.Y., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 22 row: F column: 06

High quality sequence stop: 543.

Location/Qualifiers

1..543

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="L7N800102s1-22-F06"

/sex="M"

/lab_host="Top10F"

/clone_lib="L7N800102s1"

/note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;

Site_2: NotI; The poly (A) + RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then deacapped

with tobacco acid pyrophosphatase (TAP). The deacapped

intact mRNA was ligated with DNA-RNA linker including

EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and Nid114 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

ORIGIN

Alignment Scores:

Pred. No.: 3,466-28
Score: 296.00
Percent Similarity: 92.73%
Best Local Similarity: 92.73%
Query Match: 89.97%
DB: 6

Length: 543
Matches: 51
Conservative: 0
Mismatches: 4
Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x CB144250 (1-543)

QY 2 AlaCysAenLeuProIleValaArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 319 GCCTGCATCTCCCATACCTCCGCGGCCCCCTCCAGCCTTATCCAGCTCGGCGATT 378
QY 22 AepAlaValIlyGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 379 GATGCTGTCAGAGGAGAGTGGCTCTCTCCCTACGCGGCGCTGCACAGGCAACGGAAC 438
QY 42 LysPheTyrSerGlyLysGlyCysArgGlyLysGlyValPro 56
DB 439 AAGTCTTACTCAGAGAGAGTGCAGAGTACTGCGGTGCTCCT 483

RESULT 13

CB148803 543 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0205202 L7N800102s1 Homo sapiens cDNA clone L7N800102s1-21-B07
DEFINITION 5', mRNA sequence.

ACCESSION CB148803
VERSION CB148803.1 GI:28131454
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 543)
AUTHORS Kim N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Kim, K.J., Cheong, D.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr

Plate: 21 row: B column: 07
High quality sequence stop: 543.
Location/Qualifiers
1. 543
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L7N800102s1-21-B07"
/sex="M"
/lab_host="Top10F"
/clone_lib="L7N800102s1"

/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphorylated with tobacco acid pyrophosphatase (TAP). The dephosphorylated intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and Nid114 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

ORIGIN

Alignment Scores:

Pred. No.: 3,466-28
Score: 296.00
Percent Similarity: 92.73%
Best Local Similarity: 92.73%
Query Match: 89.97%
DB: 6

Length: 543
Matches: 51
Conservative: 0
Mismatches: 4
Indels: 0
Gaps: 0

US-10-038-722-27 (1-56) x CB148803 (1-543)

QY 2 AlaCysAenLeuProIleValaArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 319 GCCTGCATCTCCCATACCTCCGCGGCCCCCTCCAGCCTTATCCAGCTCGGCGATT 378
QY 22 AepAlaValIlyGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
DB 379 GATGCTGTCAGAGGAGAGTGGCTCTCTCCCTACGCGGCGCTGCACAGGCAACGGAAC 438
QY 42 LysPheTyrSerGlyLysGlyCysArgGlyLysGlyValPro 56
DB 439 AAGTCTTACTCAGAGAGAGTGCAGAGTACTGCGGTGCTCCT 483

RESULT 14

AI193912 550 bp mRNA linear EST 29-OCT-1998
LOCUS AI193912/C
DEFINITION qe73b01.x1 Soares fetal lung Nblh19w Homo sapiens cDNA clone IMAGE:1744585 3' similar to gb:X04225 ALPBA-1-MICROGLOBULIN (HUMAN);, mRNA sequence.
ACCESSION AI193912
VERSION AI193912.1 GI:3745121
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 550)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-r@mail.nih.gov
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 643 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 337.
FEATURES
 source
 1..550
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1744585"
 /dev_stage="19 weeks"
 /lab_host="PH10B (ampicillin resistant)"
 /clone_lib="Soares fetal lung NBHL19W"
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTCACATCTGAGATGGAGGAGGCGCCCATTTTCTTTTCTT-3'] double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."

ORIGIN
 Alignment Scores:
 Pred. No.: 3,52e-28 Length: 550
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0
 US-10-038-722-27 (1-56) x AI193912 (1-550)
 QY 2 AAlaCyAsnLeuProIleValArgGlyProCyAlleAlaPhePheProArgTrpAlaPhe 21
 Db 316 GCGTCAATCTCCCATATGTCGGGGCCCTGCGAGCCTTCATCCAGCTCTGGGCAATT 257
 QY 22 AspAlaValIlyGlyCyValLeuPheProTyGlyGlyCyGlnGlyAangIyAan 41
 Db 256 GATGCTGTCAAGGGGAGAGTGGCTCTTCCCTACGGGGGGTGCAGGGCAACGGGAAC 197
 QY 42 LysPheTySerGluIyGlyCyAangIyCyAangIyCyGlyValPro 56
 Db 196 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCCT 152
RESULT 15
 AI207590/c 571 bp mRNA linear EST 11-NOV-1999
LOCUS HA2594 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION AI207590
VERSION AI207590.1 GI:6361600
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 571)
 Yu, Y., Zhang, C., Luo, L., Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M. and He, F.
AUTHORS Expression profile analysis of a human fetal liver cDNA library
TITLE Unpublished (1998)
JOURNAL Contact: Chenggang Zhang
COMMENT Beijing Institute of Radiation Medicine
 27 Taiping Road, Beijing 100850, P.R.China
 Email: zhang_chenggang@hotmail.com.
FEATURES
 source
 1..571
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="liver"
 /dev_stage="fetal"
 /lab_host="MC1061/P3"
 /clone_lib="Human fetal liver cDNA library"
 /note="Vector: pCDNA1"
ORIGIN
 Alignment Scores:
 Pred. No.: 3,69e-28 Length: 571
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0
 US-10-038-722-27 (1-56) x AI207590 (1-571)
 QY 2 AAlaCyAsnLeuProIleValArgGlyProCyAlleAlaPhePheProArgTrpAlaPhe 21
 Db 316 GCGTCAATCTCCCATATGTCGGGGCCCTGCGAGCCTTCATCCAGCTCTGGGCAATT 257
 QY 22 AspAlaValIlyGlyCyValLeuPheProTyGlyGlyCyGlnGlyAangIyAan 41
 Db 256 GATGCTGTCAAGGGGAGAGTGGCTCTTCCCTACGGGGGGTGCAGGGCAACGGGAAC 197
 QY 42 LysPheTySerGluIyGlyCyAangIyCyAangIyCyGlyValPro 56
 Db 196 AAGTCTACTCAGAGAGAGTGCAGAGTACTGCGGTGTCCCT 152
RESULT 16
 AI336247/c 583 bp mRNA linear EST 13-FEB-1999
LOCUS q45b07.x1 Soares_fetal_lung NBHL19W Homo sapiens cDNA clone
 IMAGE:1950901 3' similar to gp:X04225 ALPFA-1-WICKROGLOBULIN
 (HUMAN); mRNA sequence.
DEFINITION sequence.
ACCESSION AI336247
VERSION AI336247.1 GI:4073174
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 583)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-r@mail.nih.gov
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 833 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 297.
FEATURES
 source
 1..583
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

/clone="IMAGE:1950901"
/dev stage="19 weeks"
/lab host="DH10B (ampicillin resistant)"
/clone.lib="Soares_fetal_lung_NbH19W"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT-3'] double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH19W."

ORIGIN

Alignment Scores:

Pred. No.:	3,79e-28	Length:	583
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x A1336247 (1-583)

QY 2 A1aCyaaenleuproilevalarglyprocyalllealaphpheproargtrpalaphe 21
Db 319 GCTTCACATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTTGCGCATTT 260
QY 22 Aapalavalllysglylyscyvalleupheprotyrglyglycyglnllyasnglyasn 41
Db 229 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGCGGGGCTGCGAGGCGAAC 200
QY 42 LysPheTYrSerGluLysGluCyaaArglyurtyrCygslyvalpro 56
Db 199 AAGTTTACTCAGAGAGAGTGCAGAGTACTCGGTGTCCCT 155

RESULT 17

AV683002 617 bp mRNA linear EST 16-JAN-2002
LOCUS AV683002 GKC Homo sapiens cDNA clone GKCBB06 5', mRNA sequence.
ACCESSION AV683002
VERSION AV683002.1 GI:10284865
KEYWORDS EST.

ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 617)
XU,X., HUANG,J., XU,Z., QIAN,B., ZHU,Z., YAN,Q., CAI,T., ZHANG,X.,
XIAO,H., QU,J., LIU,F., HUANG,Q., CHENG,Z., LI,N., DU,J., HU,W.,
SHEN,K., LU,G., FU,G., ZHONG,M., XU,S., GU,W., HUANG,W., ZHAO,X.,
HU,G., GU,J., CHEN,Z. and HAN,Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456

COMMENT

Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..617
/organism="Homo sapiens"

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCBB06"
/tissue_type="hepatocellular carcinoma"
/dev stage="adult"
/lab host="SOLR"
/clone.lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

Alignment Scores:

Pred. No.:	4.07e-28	Length:	617
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x AV683002 (1-617)

QY 2 A1aCyaaenleuproilevalarglyprocyalllealaphpheproargtrpalaphe 21
Db 59 GCTTCACATCTCCCATAGTCCGGGGCCCTCCGAGCCTTCATCCAGCTTGCGCATTT 118
QY 22 Aapalavalllysglylyscyvalleupheprotyrglyglycyglnllyasnglyasn 41
Db 119 GATGCTGTCAGAGGGAAGTGGCTCTCTCCCTACGCGGGGCTGCGAGGCGAAC 178
QY 42 LysPheTYrSerGluLysGluCyaaArglyurtyrCygslyvalpro 56
Db 179 AAGTTTACTCAGAGAGAGTGCAGAGTACTCGGTGTCCCT 223

RESULT 18

A1807643 644 bp mRNA linear EST 19-DEC-1999
LOCUS A1807643/c
DEFINITION w49d04.x1 Soares NFL T GBC_S1 Homo sapiens cDNA clone
IMAGE:2358919 3' similar to gb:X04225 ALPHA-1-MICROGLOBULIN
(HUMAN); mRNA sequence.

ACCESSION A1807643
VERSION A1807643.1 GI:5394209
KEYWORDS EST.

ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 644)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

TITLE Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1328 Std Error: 0.00
Seq primer: -40bp from Gibco
High quality sequence stop: 462.
Location/Qualifiers
1..644
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2358919"
/lab host="DH10B"
/clone.lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbH19W, testis NHR, and B-cell
NCI-GAP-GCB1) were mixed, and ss circles NHR, and B-cell
in vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731359. Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	4,296-28	Length:	644
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	0
Query Match:	89.97%	Indels:	4
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x A1807643 (1-644)

QY 2 A1ACyAsnLeuProIleValArgGlyProCySilleAlaPhePheProArgTIPAlaPhe 21
 DB 313 GCCTCAATCTCCCATAGTCCGGGCCCCCTCCGAGCTTCATCCAGCTCGGCATT 254
 QY 22 AaPa1aVal1ySg1yLysCySVal1eupheProTyrg1yG1yCySg1ng1yAa1yAa 41
 DB 253 GATGCTGTCAGAGGAGAGTGCCTCTCTCCCTACGGGGGCTGCGAGGCAACGGGAAAC 194
 QY 42 LysPheTySerG1yLysG1yCySargG1yTyrcySg1yValPro 56
 DB 193 AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTCGGCTGTCTCT 149

RESULT 19
 AV686492 670 bp mRNA linear EST 16-JAN-2002
 LOCUS AV686492 GKC Homo sapiens cDNA clone GKCNF08 5', mRNA sequence.
 DEFINITION
 AV686492.1 GI:10288355
 VERSION
 AV686492.1 GI:10288355
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1 (baaes 1 to 670)
 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Ou,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z. and Han,Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Contract: Zenguan Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@hgc.sh.cn
 This clone is available at CHGC in Shanghai.
 Location/Qualifiers

FEATURES

source

1..670
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKCNF08"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GKC"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	4,516-28	Length:	670
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4
Query Match:	89.97%	Indels:	0
DB:	1	Gaps:	0

US-10-038-722-27 (1-56) x AV686492 (1-670)

QY 2 A1ACyAsnLeuProIleValArgGlyProCySilleAlaPhePheProArgTIPAlaPhe 21
 DB 95 GCCTCAATCTCCCATAGTCCGGGCCCCCTCCGAGCTTCATCCAGCTCGGCATT 154
 QY 22 AaPa1aVal1ySg1yLysCySVal1eupheProTyrg1yG1yCySg1ng1yAa1yAa 41
 DB 155 GATGCTGTCAGAGGAGAGTGCCTCTCTCCCTACGGGGGCTGCGAGGCAACGGGAAAC 214
 QY 42 LysPheTySerG1yLysG1yCySargG1yTyrcySg1yValPro 56
 DB 215 AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTCGGCTGTCTCT 259

RESULT 20
 A173259/c 675 bp mRNA linear EST 16-NOV-1999
 LOCUS A173259/c
 DEFINITION
 X155C08.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
 IMAGE:2664014 3' similar to gb:X04225 ALPFA-1-MICROGLOBULIN
 (HUMAN); mRNA sequence.
 ACCESSION
 A173259
 VERSION
 A173259.1 GI:6439207
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1 (baaes 1 to 675)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rtmail.nih.gov
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40UP from G1bco
 High quality sequence stop: 461.
 Location/Qualifiers

FEATURES

source

1..675
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2664014"
 /lab_host="BDH10B"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI-CGAP GCBI) were mixed and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731359. Subtraction by Bento
 Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	4,566-28	Length:	675
Score:	296.00	Matches:	51
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	4

ORIGIN

Query Match: 89.97% Indels: 0
DB: 2 Gaps: 0
US-10-038-722-27 (1-56) x AM173259 (1-675)

QY 2 AAlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 312 GCCTCAATCTCCCATAGTCCGGGGCCCTGCCGAGCTTCATCCAGCTCTGGGCAATT 253

QY 22 AApAlaValIyGlyGlyCyValLeuPheProTyTrGlyGlyCyGlnGlyAsnGlyAsn 41
DB 252 GATGCTGTCAAGGGAGAGTGGCTCTTCCCTACGGGGGCTGCGCAGGGCAACGGGAAAC 193

QY 42 LysPheTySerGluTyGluGlyCysArgGluTyTrCysGlyValPro 56
DB 192 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTCTCCT 148

RESULT 21
AV686493 682 bp mRNA linear EST 16-JAN-2002
LOCUS AV686493 GKC Homo sapiens cDNA clone GKCENF09 5', mRNA sequence.
DEFINITION AV686493
ACCESSION AV686493.1 GI:10288356
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCENF09"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Alignment Scores: 4.62e-28 Length: 682
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
US-10-038-722-27 (1-56) x AV686493 (1-682)

QY 2 AAlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 312 GCCTCAATCTCCCATAGTCCGGGGCCCTGCCGAGCTTCATCCAGCTCTGGGCAATT 253

DB 95 GCCTCAATCTCCCATAGTCCGGGGCCCTGCCGAGCTTCATCCAGCTCTGGGCAATT 154
QY 22 AApAlaValIyGlyGlyCyValLeuPheProTyTrGlyGlyCyGlnGlyAsnGlyAsn 41
DB 155 GATGCTGTCAAGGGAGAGTGGCTCTTCCCTACGGGGGCTGCGCAGGGCAACGGGAAAC 214

QY 42 LysPheTySerGluTyGluGlyCysArgGluTyTrCysGlyValPro 56
DB 215 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGCGGTCTCCT 259

RESULT 22
AV645324 683 bp mRNA linear EST 15-JAN-2002
LOCUS AV645324 GUA Homo sapiens cDNA clone GLAAB01 3', mRNA sequence.
DEFINITION AV645324
ACCESSION AV645324
VERSION AV645324.1 GI:9866338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 683)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..683
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLAAB01"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GUA"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Alignment Scores: 4.62e-28 Length: 683
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
US-10-038-722-27 (1-56) x AV645324 (1-683)

QY 2 AAlaCyAsnLeuProIleValArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
DB 296 GCCTCAATCTCCCATAGTCCGGGGCCCTGCCGAGCTTCATCCAGCTCTGGGCAATT 237

QY 22 AApAlaValIyGlyGlyCyValLeuPheProTyTrGlyGlyCyGlnGlyAsnGlyAsn 41
DB 236 GATGCTGTCAAGGGAGAGTGGCTCTTCCCTACGGGGGCTGCGCAGGGCAACGGGAAAC 177

QY 42 LysPheTySerGluTyGluGlyCysArgGluTyTrCysGlyValPro 56

Db 176 AAGTCTACTCAGAGAAGAGTGACAGAGTACTGCGGTGCTCCT 132

RESULT 23
LOCUS AV700236/c
DEFINITION AV700236 GKC Homo sapiens cDNA clone GKCRD11 3', mRNA sequence.
ACCESSION AV700236
VERSION AV700236.1 GI:10302207
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 687)
Xia, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Shen, K., Lu, G., Fu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
JOURNAL 21625106
MEDLINE 11752456
PUBMED
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCRD11"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 4.66e-28 Length: 687
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV700236 (1-687)

QY 2 AAlaCyASnLeuProIleValArgIyProCyAlleAlaPheProArgTrpAlaPhe 21
|||||
Db 306 GCGTGAATCTCCCAATAGTCGGGGCCCTGCGAGCTTCATCCAGCTCTGGGCATT 247
|||||
QY 22 AAPAlaValIyEGlyLysCySValIleuPheProTyrGlyGlyCySGInGlyAsnGlyAsn 41
|||||
Db 246 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTCAGGGGGGCTCCAGGGCAACGGGAAC 187
|||||
QY 42 LysPheTyrSerGluLysGluCySArgIyTyrCySGIyValPro 56
|||||
Db 186 AAGTCTACTCAGAGAAGAGTGACAGAGTACTGCGGTGCTCCT 142
|||||

RESULT 24
LOCUS AV645372/c
DEFINITION AV645372 GUA Homo sapiens cDNA clone GLAAAF01 3', mRNA sequence.

ACCESSION AV645372
VERSION AV645372.1 GI:9866386
EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 692)
Xia, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Shen, K., Lu, G., Fu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
JOURNAL 21625106
MEDLINE 11752456
PUBMED
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..692
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLAAAF01"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GLA"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 4.7e-28 Length: 692
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x AV645372 (1-692)

QY 2 AAlaCyASnLeuProIleValArgIyProCyAlleAlaPheProArgTrpAlaPhe 21
|||||
Db 297 GCGTGAATCTCCCAATAGTCGGGGCCCTGCGAGCTTCATCCAGCTCTGGGCATT 238
|||||
QY 22 AAPAlaValIyEGlyLysCySValIleuPheProTyrGlyGlyCySGInGlyAsnGlyAsn 41
|||||
Db 237 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTCAGGGGGGCTCCAGGGCAACGGGAAC 178
|||||
QY 42 LysPheTyrSerGluLysGluCySArgIyTyrCySGIyValPro 56
|||||
Db 177 AAGTCTACTCAGAGAAGAGTGACAGAGTACTGCGGTGCTCCT 133
|||||

RESULT 25
LOCUS BU689265/c
DEFINITION BU689265 692 bp mRNA linear EST 07-OCT-2002
UI-CF-EC1-adw-b-01-0-UI.81 UI-CF-EC1 Homo sapiens cDNA clone
ACCESSION BU689265
VERSION BU689265
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 04:19:32 ; Search time 138 Seconds
(without alignments)
663.996 Million cell updates/sec

Title: US-10-038-722-27

Perfect score: 329
Sequence: 1 EACNLPIVRCPCIAFPFPRWA.....QGNGKFKYSEKREYCGVP 56

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cg2_1/USPTO.spool/US10038722/runat_18022005_145236_14347/app_query_fastq_1.139
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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR MAX=100 -THR MIN=0 -ALIGN=25
-MODE=LOCAL -OUTPMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10038722 @CGN 1 1 177 @runat_18022005_145236_14347 -NCPu=6 -ICP=3
-NO_MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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2:	/cg2_6/ptodata/1/ina/5B.COMB.seq:*
3:	/cg2_6/ptodata/1/ina/6A.COMB.seq:*
4:	/cg2_6/ptodata/1/ina/6B.COMB.seq:*
5:	/cg2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6:	/cg2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	448	1	US-08-358-160-68
2	324	98.5	8584	1	US-08-358-160-66
3	324	98.5	8590	1	US-08-358-160-70
4	296	90.0	198	1	US-07-791-213D-12
5	296	90.0	198	1	US-08-293-150A-12
6	296	90.0	204	4	US-09-331-793-27
7	296	90.0	204	4	US-07-791-213D-15
8	296	90.0	209	1	US-08-293-150A-15
9	296	90.0	210	1	US-07-791-213D-11
10	296	90.0	210	1	US-07-972-387-74
11	296	90.0	210	1	US-08-431-412-74
12	296	90.0	210	1	US-08-057-971-74

13	296	90.0	210	1	US-08-293-150A-11
14	296	90.0	210	2	US-08-235-515A-24
15	296	90.0	295	1	US-07-791-213D-85
16	296	90.0	295	1	US-08-293-150A-85
17	296	90.0	313	1	US-07-791-213D-75
18	296	90.0	313	1	US-08-293-150A-75
19	296	90.0	343	2	US-08-235-515A-28
20	296	90.0	344	1	US-07-972-387-13
21	296	90.0	344	1	US-08-431-412-13
22	296	90.0	344	1	US-08-057-971-13
23	296	90.0	349	1	US-07-972-387-3
24	296	90.0	349	1	US-08-431-412-3
25	296	90.0	349	1	US-08-057-971-3
26	296	90.0	350	1	US-07-791-213D-92
27	296	90.0	350	1	US-08-293-150A-92
28	296	90.0	441	4	US-09-331-793-28
29	296	90.0	624	4	US-09-101-272G-79
30	296	90.0	645	4	US-09-101-272G-95
31	296	90.0	666	4	US-09-101-272G-97
32	295	89.7	343	1	US-07-972-387-5
33	295	89.7	343	1	US-08-431-412-5
34	295	89.7	343	1	US-08-057-971-5
35	294	89.4	240	4	US-09-101-272G-75
36	294	89.4	253	4	US-09-101-272G-16
37	294	89.4	259	1	US-08-325-243A-2
38	294	89.4	261	4	US-09-101-272G-17
39	287	87.2	210	1	US-07-791-213D-14
40	287	87.2	210	1	US-08-293-150A-14
41	287	87.2	313	1	US-07-791-213D-88
42	287	87.2	313	1	US-07-972-387-1
43	287	87.2	313	1	US-08-431-412-1
44	287	87.2	313	1	US-08-057-971-1
45	287	87.2	313	1	US-08-293-150A-88

ALIGNMENTS

RESULT 1
US-08-358-160-68
Sequence 68, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: synthetic DNA fragment
US-08-358-160-68

Alignment Scores:
Pred. No.: 1,9e-39 Length: 448
Score: 329.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-358-160-68 (1-448)

QY 1 GUAACyAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrPa 20
DB 265 GAGGCTTGAATTGCGCATGCTCAGAGTCCATGATGCTTCTCCCAAGATGGCGT 324
QY 21 PheAspAlaValIleGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 40
DB 325 TTCGACGCTGTAAAGGTAAGTGGCTGTTCCTCCATCAGGTGGTGTCAAGGTAAAGCGT 384
QY 41 AsnLysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 385 AACAACTTACTCTGAGAGAGGTGTAGAGAGTACTGTGTGTCCA 432

RESULT 2

US-08-358-160-66
Sequence 66, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 8584 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: DNA plasmid
US-08-358-160-66

Alignment Scores:
Pred. No.: 6,23e-37 Length: 8584
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-358-160-66 (1-8584)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrrPa 21
DB 1212 GCTTGAATTGCGCATGCTCAGAGTCCATGATGCTTCTCCCAAGATGGCGTTC 1271
QY 22 AspAlaValIleGlyCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGly 41
DB 1272 GACGCTGTAAAGGTAAGTGGCTGTTCCTCCATCAGGTGGTGTCAAGGTAAAGCGTAAAC 1331
QY 42 LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro 56
DB 1332 AAGTCTACTCTGAGAGAGGTGTAGAGAGTACTGTGTGTCCA 1376

RESULT 3

US-08-358-160-70
Sequence 70, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEV=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 8590 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: DNA plasmid
US-08-358-160-70
Alignment Scores:
Pred. No.: 6.24e-37 Length: 8590
Score: 324.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-08-358-160-70 (1-8590)
QY 2 AlaCySaenLeupProIleValaIArgGlyProCySilealaphnePheProArgTTPalalphe 21
DB 1212 GCTTCTACTCTGCAATGCTGTCAGAGGTCATGCTTCTTCCCAAGATGGGCTTTC 1271
QY 22 AspaIaValIySgIyLysCySaValLeupheProTyrgIyGlyCySgInGlyASngIyASn 41
DB 1272 GACCGTGTAAAGGTAAGGCGCTTGTTCCTATCGGAGTGTGCAAGGTAAAGGTAAAC 1331
QY 42 LysPheTySerGluLysGluCySaArgGluTyrcySgIyValPro 56
DB 1332 AAGTTCTACTCTGAGAAAGAGTGTAGAGAGTGTGTGTTCCA 1376

RESULT 4
US-07-791-213D-12
Sequence 12, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 108
TITLE OF INVENTION: TREATING USING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-12
Alignment Scores:
Pred. No.: 4.69e-35 Length: 198
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0
US-10-038-722-27 (1-56) x US-07-791-213D-12 (1-198)
QY 2 AlaCySaenLeupProIleValaIArgGlyProCySilealaphnePheProArgTTPalalphe 21
DB 10 GCTGCAATCTCCCATGTCGCGGGCCCTGCGAGCTTCATCCAGCTCTGGGCAATTT 69
QY 22 AspaIaValIySgIyLysCySaValLeupheProTyrgIyGlyCySgInGlyASngIyASn 41
DB 70 GATGCTGCAAGGGAAGATGCTCTCTTCCCTTACGGGGGCTGCAAGGCAACGGGAAC 129
QY 42 LysPheTySerGluLysGluCySaArgGluTyrcySgIyValPro 56
DB 130 AAGTTCTACTCTGAGAAAGAGTGTAGAGAGTGTGTGTTCCCT 174
RESULT 5
US-08-293-150A-12
Sequence 12, Application US/08293150A

```

: Patent No. 5792629
:
: GENERAL INFORMATION:
: APPLICANT: MORISHITA, Hideaki
: APPLICANT: KANAMORI, Toshimori
: APPLICANT: NOBUHARA, Masahiro
: TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
: TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
: TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
: NUMBER OF INVENTIONS: 110
: NUMBER OF SEQUENCES: 110
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DONNE, SWECKER & MATHIS
: STREET: P.O. Box 1404
: City: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/293,150A
: FILING DATE: 19-NOV-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/791,213
: FILING DATE: 13-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 2-306745
: FILING DATE: 13-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Meuth, Donna M.
: REGISTRATION NUMBER: 36,607
: REFERENCE/DOCKET NUMBER: 029650-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 198 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-293-150A-12
:
: Alignment Scores:
: Pred. No: 4.69e-35 length: 198
: Score: 296.00 Matches: 51
: Percent Similarity: 92.73% Conservative: 4
: Best local Similarity: 92.73% Mismatches: 4
: Query Match: 89.97% Indels: 0
: DB: 1 Gaps: 0
:
: US-10-038-722-27 (1-56) x US-08-293-150A-12 (1-198)
:
: Oy 2 AlaCysAsnLeuProIleValAlaArgGlyProCysIleAlaPheProArgTrpAlaPhe 21
: Db 10 GCCGCGAATCTCCCATAGTCGCGGGGCCCTCCGACGCTTATCCACACTCTGGGCAATT 69
:
: Oy 22 AspaValAlaLysGlyLysCysValLeuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
: Db 70 GATGCTGTCAAGGGGAAGTGCTGCTCTTCCCTACGGGGGGCTGCCAGGGCAACGGGAA 125
:
: Oy 42 LysPheTyrSerGlnLysGlyLysCysArgGlyLysTyrCysGlyValPro 56
: Db 130 AAGTTCTACTCAGAGGAAGAGTGCAGAGAGTACTGGGATGTCCT 174
:
: RESULT 6
: US-09-331-793-27
: Sequence 27, Application US/09331793

```

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Patent No. 6500646
GENERAL INFORMATION:
APPLICANT: KIRIYAMA, Shinichi
APPLICANT: HASSEGAWA, Takaichi
TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
FILE REFERENCE: 1110-253P
CURRENT APPLICATION NUMBER: US/09/331,793
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 204
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-331-793-27

Alignment Scores:
Pred. No.: 4,88e-35 Length: 204
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 4 Gaps: 0

US-10-038-722-27 (1-56) x US-09-331-793-27 (1-204)

Qy 2 ALGCAASHLEUPROLEVALRGELYPROCYSTLEALAPHEPHEPROARGTTPALAPHE 21
Db 4 GCGTCGAACCTCCCACTACCTCCGGGGCCCTGCGAGCCTTCATCCAGCTCTGGGCATT 63

Qy 22 ASDALVALYRGELYLYSCYSAVALLEUPHEPROTYRGILGYLYCYSGINGLYAENGLYASN 41
Db 64 GATGCTGTCAAGGGAGAGTGCCTCTCTTCCCTACGGGGGCTGCGAGGCAACGGGAC 122

Qy 42 LYSPHETYSERGIULYSGINUCYSAARGELUTRYCYSGILYVALPRO 56
Db 124 AAGTCTACTACAGAGAGAGTGCAGAGAGTACTCGGTGTCCT 168

RESULT 7
US-07-791-213D-15
Sequence 15, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahito
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607

```

REFERENCE/DOCKET NUMBER: 029650-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 209 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-07-791-213D-15

Alignment Scores:
 Pred. No.: 5,05e-35 Length: 209
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-791-213D-15 (1-209)

Qy 2 AlaCysAenLeuProIleValAlaArgIleAlaPheProArgTrrAlaPhe 21
 Db 10 GCTGCAATCTCCCATAGTCCGGGCCCCCTGCCAGCCTTCATCAAGCTCGGCATTT 69
 Qy 22 AspaIaValIyGlyVlyGlyCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 Db 70 GATGCTGTCAGAGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCGCAGGGCAACGGGAAC 129
 Qy 42 LysPheTyrSerGluIyGlyGluCysArgGluTyrCysGlyValPro 56
 Db 130 AAGTTCTACTCAGAGAGAGAGTGCAGAGAGTACTGCGGTGTCTCT 174

RESULT 8
 US-08-293-150A-15
 Sequence 15, Application US/08293150A
 Patent No. 5792629

GENERAL INFORMATION:
 APPLICANT: MORISHITA, Hideaki
 APPLICANT: KANAMORI, Toshinori
 APPLICANT: NOBUHARA, Masahiro
 TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
 TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
 TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 TITLE OF INVENTION: TREATING USING THE SAME
 NUMBER OF SEQUENCES: 110
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/293,150A
 FILING DATE: 19-AUG-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/791,213
 FILING DATE: 13-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 2-306745
 FILING DATE: 13-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Meuth, Donna M.
 REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 029650-049
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 209 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-293-150A-15

Alignment Scores:
 Pred. No.: 5,05e-35 Length: 209
 Score: 296.00 Matches: 51
 Percent Similarity: 92.73% Conservative: 0
 Best Local Similarity: 92.73% Mismatches: 4
 Query Match: 89.97% Indels: 0
 DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-293-150A-15 (1-209)

Qy 2 AlaCysAenLeuProIleValAlaArgIleAlaPheProArgTrrAlaPhe 21
 Db 10 GCTGCAATCTCCCATAGTCCGGGCCCCCTGCCAGCCTTCATCAAGCTCGGCATTT 69
 Qy 22 AspaIaValIyGlyVlyGlyCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
 Db 70 GATGCTGTCAGAGGGAGAGTGGCTCTCTCCCTACGGGGGGCTGCGCAGGGCAACGGGAAC 129
 Qy 42 LysPheTyrSerGluIyGlyGluCysArgGluTyrCysGlyValPro 56
 Db 130 AAGTTCTACTCAGAGAGAGAGTGCAGAGAGTACTGCGGTGTCTCT 174

RESULT 9
 US-07-791-213D-11
 Sequence 11, Application US/07791213D
 Patent No. 5409695

GENERAL INFORMATION:
 APPLICANT: MORISHITA, Hideaki
 APPLICANT: KANAMORI, Toshinori
 APPLICANT: NOBUHARA, Masahiro
 TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
 TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
 TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 TITLE OF INVENTION: TREATING USING THE SAME
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/791,213D
 FILING DATE: 13-NOV-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 2-306745
 FILING DATE: 13-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Meuth, Donna M.
 REGISTRATION NUMBER: 36,607
 REFERENCE/DOCKET NUMBER: 029650-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-11

Alignment Scores:
Pred. No.: 5.08e-35 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-791-213D-11 (1-210)

QY 2 AlaCyseAmLeuProIleValArgGlyProCySileAlaPhePheProArgTrrAlaPhe 21
Db 10 GCTCTCAATCTCCCATATGTCGGGGCCCCCTGCCAGACCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIyGlyVlyCyseValIeuPheProTYrGlyGlyCySgInGlyAsnGlyAsn 41
Db 70 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTTACGGGGGCTGCCAGGGCAACGGGAAC 129

QY 42 LysPheTYrSerGluLysGluCyseArgGlyIuTYrCySgIyValPro 56
Db 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGGCGGTGCCCT 174

RESULT 10
US-07-972-387-74
; Sequence 74, Application US/07972387
; Patent No. 5451659
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshinori
; APPLICANT: No. 5451659hara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,387
; FILING DATE: 19921105
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ. ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..210
; OTHER INFORMATION: /label= sequence
; OTHER INFORMATION: /note= "encodes TN70 polypeptide"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..210
US-07-972-387-74

Alignment Scores:
Pred. No.: 5.08e-35 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-972-387-74 (1-210)

QY 2 AlaCyseAmLeuProIleValArgGlyProCySileAlaPhePheProArgTrrAlaPhe 21
Db 10 GCTCTCAATCTCCCATATGTCGGGGCCCCCTGCCAGACCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIyGlyVlyCyseValIeuPheProTYrGlyGlyCySgInGlyAsnGlyAsn 41
Db 70 GATGCTGTCAAGGGAGAGTGGCTCTCTCCCTTACGGGGGCTGCCAGGGCAACGGGAAC 129

QY 42 LysPheTYrSerGluLysGluCyseArgGlyIuTYrCySgIyValPro 56
Db 130 AAGTCTACTCAGAGAGAGTGCAGAGAGTACTGGCGGTGCCCT 174

RESULT 11
US-08-431-412-74
; Sequence 74, Application US/08431412
; Patent No. 5589360
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshinori
; APPLICANT: No. 5589360hara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,412
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/972,387
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300

TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: -
LOCATION: 1..210
OTHER INFORMATION: /label= sequence
OTHER INFORMATION: /note="encodes TN70 polypeptide"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..210
US-08-431-412-74

Alignment Scores:
Pred. No.: 5,08e-35 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-431-412-74 (1-210)

QY 2 AlaCysAenLeuProIleValArgIleProCysIleAlaPheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCGCGGCCCCCTGCGAGCCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIyGlyIyGlyCysValIeupheProTyrgIyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGCAAGGGGAGAGTGGCTCTTCCCTACGGGGGCTGCGAGGGCAACGGGAAAC 129

QY 42 LysPheTySerGluIyGlyGluCysArgGluTyrcysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGAGTGCAGAGATCTCGGTGTCCT 174

RESULT 12
US-08-057-971-74
Sequence 74, Application US/08057971
Patent No. 5679770
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshihori
APPLICANT: No. 5679770uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/057,971
FILING DATE: 06-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.

REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-129P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: -
LOCATION: 1..210
OTHER INFORMATION: /label= sequence
OTHER INFORMATION: /note="encodes TN70 polypeptide"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..210
US-08-057-971-74

Alignment Scores:
Pred. No.: 5,08e-35 Length: 210
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-057-971-74 (1-210)

QY 2 AlaCysAenLeuProIleValArgIleProCysIleAlaPheProArgTrrAlaPhe 21
DB 10 GCTGCAATCTCCCATAGTCGCGGCCCCCTGCGAGCCTTCATCCAGCTCTGGGCATTT 69

QY 22 AspaIaValIyGlyIyGlyCysValIeupheProTyrgIyGlyCysGlnGlyAsnGlyAsn 41
DB 70 GATGCTGCAAGGGGAGAGTGGCTCTTCCCTACGGGGGCTGCGAGGGCAACGGGAAAC 129

QY 42 LysPheTySerGluIyGlyGluCysArgGluTyrcysGlyValPro 56
DB 130 AAGTCTACTCAGAGAGAGAGTGCAGAGATCTCGGTGTCCT 174

RESULT 13
US-08-293-150A-11
Sequence 11, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshihori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```

1 FILING DATE: 29-Apr-1994
2 CLASSIFICATION: 435
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Murphy Jr., Gerald M.
5 REGISTRATION NUMBER: 28,977
6 REFERENCE/DOCKET NUMBER: 1110-135P
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 703-205-8000
9 TELEFAX: 703-205-8050
10 INFORMATION FOR SEQ. ID NO: 24:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 210 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 MOLECULE TYPE: DNA
17 FEATURE:
18 NAME/KEY: -
19 LOCATION: 1..210 /label=polynucleotide
20 OTHER INFORMATION: /note="Formula 24, encodes a portion of E. coli
21 OTHER INFORMATION: /note="Formula 24, encodes a portion of E. coli
22 OTHER INFORMATION: alkaline phosphatase downstream from the signal
23 OTHER INFORMATION: peptide."
24 FEATURE:
25 NAME/KEY: CDS
26 LOCATION: 1..210
27 OTHER INFORMATION: /product="Formula 23, a portion of
28 OTHER INFORMATION: E. coli alkaline phosphatase"
29 US-08-235-515A-24
30
31 Alignment Scores:
32 Pred. No.: 5,08e-35 Length: 210
33 Score: 226.00 Matches: 51
34 Percent Similarity: 92.73% Conservative: 0
35 Best Local Similarity: 92.73% Mismatches: 4
36 Query Match: 89.97% Indels: 0
37 Gaps: 0
38
39 US-10-038-722-27 (1-56) x US-08-235-515A-24 (1-210)
40
41 QY 2 AlaCyasnlleuprollevalargslpocysilealaphpheproargtrpiala 21
42 Db 10 GCGTGAATCTCCCATATGTCGGGGCCCGGAGCTTCATCCAGCTCTGGGCAATT 69
43
44 QY 22 ASPDAIVALLYGLIYLYSCYVALLEUPHEPOTYRGIYGLIYCYGSLNGIYASNGIYASN 41
45 Db 70 GAGTGGTCAAGGGGGAAGTGCCTCTCTCCCTTACGGGGGCTGCACAGGCAACGGGAAAC 122
46
47 QY 42 LVEPHEIYSESGILYGLIYCYSAIRGIIYTCYSGIYVALPPro 56
48 Db 130 AAGTTCTTACTCAGAGAGAGTGCAGAGAGTATCTGCGGATGTCCT 174
49
50 RESULT 15
51 US-07-791-213D-85
52 Sequence 85, Application US/07791213D
53 Patent No. 540895
54 GENERAL INFORMATION:
55 APPLICANT: MORISHITA, Hideaki
56 APPLICANT: KANAMORI, Toshio
57 APPLICANT: NOBUHARA, Masahiro
58 TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
59 TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
60 TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
61 TITLE OF INVENTION: TREATING USING THE SAME
62 NUMBER OF SEQUENCES: 108
63 CORRESPONDENCE ADDRESS:
64 ADDRESSEE: Burns, Doane, Swecker & Mathis
65 STREET: P.O. Box 1404
66 CITY: Alexandria
67 STATE: Virginia
68 COUNTRY: United States
69 ZIP: 22313-1404
70
71 COMPUTER READABLE FORM:

```


COMPUTER READABLE FORM:

STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 27..303
US-07-791-213D-75

Alignment Scores:
Pred. No.: 8,84e-35 Length: 313
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-07-791-213D-75 (1-313)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 99 GCCTGCAATCTCCCATATGTCGGGGCCCTGCGAGCTTCATCCAGCTCTGGGCAATT 158

QY 22 AspaIaValIlyGlyLysCysValLeuPheProTyrgIlyGlyCysGlnGlyAsnGlyAsn 41
DB 159 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTACGGGGGCTGCCAGGGGAACGGGAAC 218

QY 42 LysPheTySerGluLysGluCysArgGluTyrcysGlyValPro 56
DB 219 AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 263

RESULT 18
US-08-293-150A-75
Sequence 75, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshihori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 27..303
US-08-293-150A-75

Alignment Scores:
Pred. No.: 8,84e-35 Length: 313
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-038-722-27 (1-56) x US-08-293-150A-75 (1-313)

QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
DB 99 GCCTGCAATCTCCCATATGTCGGGGCCCTGCGAGCTTCATCCAGCTCTGGGCAATT 158

QY 22 AspaIaValIlyGlyLysCysValLeuPheProTyrgIlyGlyCysGlnGlyAsnGlyAsn 41
DB 159 GATGCTGTCAAGGGGAAGTGCCTCTTCCCTACGGGGGCTGCCAGGGGAACGGGAAC 218

QY 42 LysPheTySerGluLysGluCysArgGluTyrcysGlyValPro 56
DB 219 AAGTCTACTCAGAGAGAGAGTGCAGAGAGTACTGCGGTGTCCT 263

RESULT 19
US-08-235-515A-28
Sequence 28, Application US/08235515A
Patent No. 5840518
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshihori
APPLICANT: No. 5840518uhara, Masahiro
TITLE OF INVENTION: DNA FRAGMENT, VECTOR CONTAINING THE DNA
TITLE OF INVENTION: FRAGMENT, TRANSFORMANT TRANSFORMED WITH THE VECTOR AND
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEIN USING THE VECTOR
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747

CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,515A
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-135P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8000
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..343
OTHER INFORMATION: /label= polynucleotide
OTHER INFORMATION: /note= "j-x1-y-z (AN68), insert in plasmid pm710,
OTHER INFORMATION: Figure 11"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 27..89
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 90..329
FEATURE:
NAME/KEY: CDS
LOCATION: 27..329
US-08-235-515A-28
Alignment Scores:
Pred. No.: 1e-34 Length: 343
Score: 296.00 Matches: 51
Percent Similarity: 92.73% Conservative: 0
Best Local Similarity: 92.73% Mismatches: 4
Query Match: 89.97% Indels: 0
Gaps: 0
DB: 2
US-10-038-722-27 (1-56) x US-08-235-515A-28 (1-343)
QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
Db 129 GCCTGTATCTACCAATATGTCGGGGCCCCCTGCCAGCCTTCATCCACTCTGGGCATTT 188
QY 22 AspaAlaValIysGlyLysCysValIleuPheProTyrGlyGlyCysGlnGlyAsnGlyAsn 41
Db 189 GATCCTGTCAAGAGGGAAGTGGCTCTCTCCCTACGGGGGAGCTGCCAGGGCAACGGGAAAC 248
QY 42 LysPheTyrSerGluValGluCysArgGluTyrCysGlyValPro 56
Db 249 AAGTTCTACTCAGAGAGAGAGTGCAGAGACTGCGGTGTCCT 293
RESULT 20
US-07-972-387-13
Sequence 13, Application US/07972387
Patent No. 5451659
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshinori

APPLICANT: No. 5451659uhara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
TITLE OF INVENTION: Producing the Same
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,387
FILING DATE: 19921105
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-124P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
STRAIN: J55055 (pMS76B)
FEATURE:
NAME/KEY: -
LOCATION: 1..344
OTHER INFORMATION: /label= sequence
OTHER INFORMATION: /note= "as in Figure 31"
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LOCATION: 44..106
OTHER INFORMATION: /standard_name= "pho A signal
OTHER INFORMATION: sequence"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 107..310
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OTHER INFORMATION: Q19K-AN"
FEATURE:
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US-07-972-387-13
Alignment Scores:
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Query Match: 89.97% Indels: 0
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QY 2 AlaCysAsnLeuProIleValArgGlyProCysIleAlaPhePheProArgTrpAlaPhe 21
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04      42  LysphetyrYserGluLysGluNcyaaArgGluIryCYsgIYvaIpro 56
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07 RESULT 21
08 US-08-431-412-13
09 ; Sequence 13, Application US/08431412
10 ; Patent No. 5589360
11 ; GENERAL INFORMATION:
12 ; APPLICANT: Morishita, Hideaki
13 ; APPLICANT: Kanamori, Toshinori
14 ; APPLICANT: No. 5589360unare, Masahiro
15 ; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
16 ; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
17 ; NUMBER OF SEQUENCES: 76
18 ; CORRESPONDENCE ADDRESS:
19 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch
20 ; STREET: 301 N. Washington St.
21 ; CITY: Falls Church
22 ; STATE: Virginia
23 ; COUNTRY: USA
24 ; ZIP: 22046-0747
25 ; COMPUTER READABLE FORM:
26 ; MEDIUM TYPE: Floppy disk
27 ; COMPUTER: IBM PC compatible
28 ; OPERATING SYSTEM: PC-DOS/MS-DOS
29 ; SOFTWARE: Patent In Release #1.0, Version #1.25
30 ; CURRENT APPLICATION DATA:
31 ; APPLICATION NUMBER: US/08/431,412
32 ; FILING DATE: 28-APR-1995
33 ; CLASSIFICATION: 435
34 ; PRIOR APPLICATION DATA:
35 ; APPLICATION NUMBER: US 07/972,387
36 ; FILING DATE: 05-NOV-1992
37 ; ATTORNEY/AGENT INFORMATION:
38 ; NAME: Murphy Jr., Gerald M.
39 ; REGISTRATION NUMBER: 28,977
40 ; REFERENCE/DOCKET NUMBER: 1110-124P
41 ; TELECOMMUNICATION INFORMATION:
42 ; TELEPHONE: 703-241-1300
43 ; TELEFAX: 703-241-2848
44 ; TEXT: 248345
45 ; INFORMATION FOR SEQ ID NO: 13:
46 ; SEQUENCE CHARACTERISTICS:
47 ; LENGTH: 344 base pairs
48 ; TYPE: nucleic acid
49 ; STRANDEDNESS: double
50 ; TOPOLOGY: linear
51 ; MOLECULE TYPE: DNA (genomic)
52 ; HYPOTHETICAL: NO
53 ; ORIGINAL SOURCE:
54 ; ORGANISM: Escherichia coli
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65 ; OTHER INFORMATION: "sequence"
66 ; FEATURE:
67 ; NAME/KEY: mat_peptide
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1 OTHER INFORMATION: Q19K-AN"
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3 NAME/KEY: CDS
4 LOCATION: 44..310
5 US-08-431-412-13
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7 Alignment Scores:
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9 Pred. No.: 1,01e-34 Length: 344
10 Score: 296.00 Matches: 51
11 Percent Similarity: 92.73% Conservative: 0
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25 Db 230 AAGTTCTACTCAGAGAGAGTGCAGAGATGTCAGATGCGGATGTCCCT 274
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27 RESULT 22
28 US-08-057-971-13
29 Sequence 13, Application US/08057971
30 Patent No.5679770
31
32 GENERAL INFORMATION:
33 APPLICANT: Morishita, Hideaki
34 APPLICANT: Kanamori, Toshinori
35 APPLICANT: No.5679770uhara, Masahiro
36 TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
37 Best of Invention: Same, Drug Composition Containing the Same and Process for
38 TITLE OF INVENTION: Producing the Same
39 NUMBER OF SEQUENCES: 81
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: Birch, Stewart, Kolasch & Birch
42 STREET: P.O. Box 747
43 CITY: Falls Church
44 STATE: Virginia
45 COUNTRY: USA
46 ZIP: 22040-0747
47
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Floppy disk
50 COMPUTER: IBM PC compatible
51 OPERATING SYSTEM: PC-DOS/MS-DOS
52 SOFTWARE: PatentIn Release #1.0, Version #1.25
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/08/057,971
55 FILING DATE: 06-MAY-1993
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57 CLASSIFICATION: 435
58 ATTORNEY/AGENT INFORMATION:
59 NAME: Murphy Jr., Gerald M.
60 REGISTRATION NUMBER: 28,977
61 REFERENCE/DOCKET NUMBER: 1110-129P
62 TELECOMMUNICATION INFORMATION:
63 TELEPHONE: 703-205-8000
64 TELEFAX: 703-205-8050
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66 TELEX:
67 INFORMATION FOR SEQ ID NO: 13:
68 SEQUENCE CHARACTERISTICS:
69 LENGTH: 344 base pairs
70 TYPE: nucleic acid
71 STRANDEDNESS: double
72 TOPOLOGY: linear
73 MOLECULE TYPE: DNA (genomic)
74 HYPOTHETICAL: NO
75 ORIGINAL SOURCE:

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; LOCATION: 107..310
; OTHER INFORMATION: /standard_name= "polypeptide"
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..310
; US-08-057-971-13
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; Pred. No.: 1.01e-34 Length: 344
; Score: 296.00 Matches: 51
; Percent Similarity: 92.73% Conservative: 0
; Best Local Similarity: 92.73% Mismatches: 4
; Query Match: 89.97% Indels: 0
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; QY 2 AlaCysAenLeuProIleValArgIlyProCysIleAlaPhePheProArgTrpAlaPhe 21
; Db 110 GCCTGATCTCAACATAGTCCGGGCCCCCTGCCAGCCTTCATCAAGCTCTGGGCATTT 169
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; QY 22 AspaIaValIySGIlybCySvaIleuPheProTyrgIyGlyCySGInGlyASnGlyAsn 41
; Db 170 GATGCTGTCAGAGGGAAGTGCCTCTTCCCTTCAGGGGGCTGCGACGGGCAACGGAAC 229
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; RESULT 23
; US-07-972-387-3
; Sequence 3, Application US/07972387
; Patent No. 5451659
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshiaki
; APPLICANT: No. 5451659hara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,387
; FILING DATE: 19921105
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Eschericia coli
; STRAIN: JE5055 (pm576)
; FEATURE:
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; LOCATION: 1..349
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; OTHER INFORMATION: /note= "as in Figure 16"
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; LOCATION: 44..106
; OTHER INFORMATION: /standard_name= "pho A signal"
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; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 107..316
; OTHER INFORMATION: /product= "polypeptide Q19K"
; FEATURE:
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; US-07-972-387-3
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; Query Match: 89.97% Indels: 0
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; RESULT 24
; US-08-431-412-3
; Sequence 3, Application US/08431412
; Patent No. 5589360
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshiaki
; APPLICANT: No. 5589360hara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
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Patent No. 5679770
GENERAL INFORMATION:
APPLICANT: Morishita, Hideaki
APPLICANT: Kanamori, Toshinori
APPLICANT: No. 5679770hara, Masahiro
TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
NUMBER OF INVENTION: Producing the Same
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Birch, Stewart, Kojasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/057,971
FILING DATE: 06-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-129P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Eschericia coli
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LOCATION: 44..106
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FEATURE:
NAME/KEY: mat_peptide
LOCATION: 107..316
OTHER INFORMATION: /product= "polypeptide Q19K"
FEATURE:
NAME/KEY: CDS
LOCATION: 44..316
US-08-057-971-3

Alignment Scores:
Pred. No.: 1.03e-34 Length: 349
Score: 296.00 Matches: 51

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Percent Similarity: 92.73%
 Best Local Similarity: 92.73%
 Query Match: 89.97%
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 Conservative: 0
 Mismatches: 4
 Indels: 0
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US-10-038-722-27 (1-56) x US-08-057-971-3 (1-349)

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Db	176	GATGCTGCAAGGGAGAGTCGCTCTTCCCTACGGGGGCTGCCAGGGCAACGGGAAC	235
Oy	42	LysPheTyrSerGluLysGluCysArgGluTyrCysGlyValPro	56
Db	236	AAGTTCTACTCAGAGAGAGAGTACGAGAGTACTGGGTGTCCCT	280

Search completed: February 23, 2005, 06:04:39
 Job time : 140 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 01:42:48 ; Search time 74 Seconds
(without alignments)
292.684 Million cell updates/sec

Title: US-10-038-722-27

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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15	329	100.0	728	8	AdR90050 Mature PD
16	329	100.0	729	7	AdF42029 DFI-14-(G
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23	324	98.5	56	8	AdF71967 Kallikrei
24	324	98.5	56	8	AdF71968 Kallikrei
25	324	98.5	141	2	AAR99214 Modified

26	307	93.3	66	2	AAR61165
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28	300	91.2	66	2	AAR61158
29	299	90.9	66	2	AAR61157
30	296	90.0	57	3	AB14179 Inter-ald
31	296	90.0	58	2	AAR78555 Human ITI
32	296	90.0	58	2	AAR81927 Human ITI
33	296	90.0	58	2	AAR81966 Human apr
34	296	90.0	58	2	AAR64116 Human Kun
35	296	90.0	58	2	AAW92863 US5880256
36	296	90.0	58	7	AdF42000 Human ITI
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38	296	90.0	58	8	AdR89983 Human ITI
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40	296	90.0	68	2	AAR65478
41	296	90.0	68	2	AAR92232
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44	296	90.0	69	2	AAR99698 Human uti
45	296	90.0	70	2	AAR65481 Protein C

ALIGNMENTS

RESULT 1
AAR99168 standard; protein; 56 AA.
ID AAR99168
AAR99168; 12-FEB-1997 (first entry)
Genetically engineered apocrotin-like Kunitz domain (EPI-HNE-4).
Aproctin; Kunitz domain; human neutrophil elastase; hNE;
connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
OS Synthetic.
PN WO9620278-A2.
PD 04-JUL-1996.
PF 15-DEC-1995; 95WO-US016349.
PR 16-DEC-1994; 94US-00358160.
(PROT-) PROTEIN ENG CORP.
"Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
WPI, 1996-321851/32.
New engineered inhibitors of human neutrophil elastase - contg. apocrotin
-like Kunitz domain for treating, e.g. cystic fibrosis or other
respiratory disorders.
Claim 1; Page 49; 105pp; English.
Genetically engineered human derived Kunitz domains can be used to
inhibit human neutrophil elastase, an enzyme involved in the elimination
of pathogens and the restructuring of connective tissue. In cases of
reduction of the circulating alpha-1-protease inhibitor (API or alpha1
antitrypsin), or the inactivation of API by oxidation (smokers
emphysema), extensive destruction of the lung tissue may result from
uncontrolled elastolytic activity of human neutrophil elastase. Other
respiratory disorders such as cystic fibrosis are thought to be caused by
human neutrophil elastase release by neutrophils. The genetically
engineered human derived Kunitz domains can be used to treat such
respiratory disorders. See AAR99146-R99211

XX
SQ Sequence 56 AA;

Query Match 100.0%; Score 329; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,4e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56

RESULT 2

ADF42070
ID ADF42070 standard; peptide; 56 AA.

XX ADF42070;

DT 12-FEB-2004 (first entry)

DE Albumin fusion protein-related DX-890 peptide.

KM albumin fusion; Kunitz domain; cytostatic; haemostatic;
KW hereditary angioedema; cancer; bleeding; gene therapy; DX-890.

XX Unidentified.

PN WO2003066824-A2.

PD 14-AUG-2003.

PF 07-FEB-2003; 2003WO-US003616.

PR 07-FEB-2002; 2002US-0355547P.

PA (AVERT) AVENTIS BEHRING GMBH.
PA (AVERT) AVENTIS BEHRING LLC.
PA (DELTA) DELTA BIOTECHNOLOGY LTD.
PA (DVAX-) DVAX CORP.

PI Hauser H, Welmer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI Ley AC;

DR WPI; 2003-731497/69.

PT Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.

PS Example 7; SEQ ID NO 20; 110pp; English.

CC The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytostatic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the albumin fusion protein-related DX-890 peptide of
CC the invention.

SQ Sequence 56 AA;

Query Match 100.0%; Score 329; DB 7; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,4e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56

RESULT 3

ADF71969
ID ADF71969 standard; protein; 56 AA.

XX ADF71969;

DT 11-MAR-2004 (first entry)

DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:49.

KM ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
KW systemic inflammatory response.

XX Homo sapiens.

PN WO2003103475-A2.

PD 18-DEC-2003.

PF 06-JUN-2003; 2003WO-US017665.

PR 07-JUN-2002; 2002US-0387239P.

PR 28-AUG-2002; 2002US-0407003P.

PA (DVAX-) DVAX CORP.

PI Ladner RC, Ley AC, Hirani S, Williams A;

DR WPI; 2004-062190/06.

PT Preventing or reducing ischemia in patient involves administering to
PT patient composition comprising a kallikrein inhibitory polypeptide.

PS Disclosure; SEQ ID NO 49; 46pp; English.

CC The present invention describes a method (M1) for preventing or reducing
CC ischaemia in a patient. M1 involves administering to the patient a
CC composition comprising a polypeptide (I) having an amino acid sequence of
CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can
CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
CC reducing ischaemia in a patient such as perioperative blood loss due to a
CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
CC is also useful for preventing or reducing the onset of systemic
CC inflammatory response associated with a surgical procedure in a patient
CC which involves administering (I) to a patient. The present sequence is
CC used in the exemplification of the present invention.

SQ Sequence 56 AA;

Query Match 100.0%; Score 329; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,4e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56
DB 1 EACNLPYVGPCTIAFFPRWAFDAVKGKCVLPFYGGCGGNGNKFYSEKCREYCGVP 56

RESULT 4

ADR90015
ID ADR90015 standard; peptide; 56 AA.

XX ADR90015;

DT 18-NOV-2004 (first entry)

DE DX-890 (an inhibitor of human neutrophil elastase) kunitz domain peptide.

KM Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytostatic; haemostatic.

XX

OS Unidentified.
 XX
 XX US2004171794-A1.
 XX
 PD 02-SEP-2004.
 XX
 XX 07-FEB-2003; 2003US-00361997.
 XX
 PR 07-FEB-2003; 2003US-00361997.
 XX
 PA (LADN/) LADNER R C.
 PA (LEYA/) LEY A C.
 XX
 PI Ladner RC, Ley AC;
 XX
 DR WPI, 2004-625120/60.
 XX
 PT New kunitz domain peptide useful as human neutrophil elastase inhibitor
 PT for the treatment of e.g. cystic fibrosis and related disease.
 XX
 PS Example 2; SEQ ID NO 40; 123pp; English.
 CC The invention relates to proteins comprising kunitz domain peptide,
 CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angioedema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cytostatic and haemostatic agent. The present sequence is a DX-890 (an
 CC inhibitor of human neutrophil elastase) kunitz domain peptide. This
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 56 AA;

Query Match 100.0%; Score 329; DB 8; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.4e-34;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EACNLPYIRGPCIAPFPFMAFDVAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
 DB 1 EACNLPYIRGPCIAPFPFMAFDVAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56

RESULT 5
 AAR9215
 ID AAR9215 standard; protein; 141 AA.
 XX
 AC AAR9215;
 XX
 DT 14-FEB-1997 (first entry)
 DE Modified Kunitz domain EPI-HNE-4.
 XX
 KW Apocitin; Kunitz domain; human neutrophil elastase; hNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
 KW smoke; emphysema.
 XX
 OS Synthetic.
 OS
 PN WO9620278-A2.
 XX
 PD 04-JUL-1996.
 XX
 PF 15-DEC-1995; 95WO-US016349.
 XX
 PR 16-DEC-1994; 94US-00358160.
 XX
 PA (PROT-) PROTEIN ENG CORP.
 XX
 PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB,
 XX WPI, 1996-321851/32.
 DR

DR N-PSDB; AAT35168.
 XX
 XX New engineered inhibitors of human neutrophil elastase - contg. aproctinin
 PT -like kunitz domain for treating, e.g. cystic fibrosis or other
 PT respiratory disorders.
 XX
 XX Claim 1; Page 68-75; 105pp; English.
 XX

CC Genetically engineered human derived kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the elimination
 CC of pathogens and the restructuring of connective tissue. In cases of
 CC reduction of the circulating alpha-1-protease inhibitor (API or alpha1
 CC antitrypsin), or the inactivation of API by oxidation (smokers
 CC emphysema), extensive destruction of the lung tissue may result from
 CC uncontrolled elastolytic activity of human neutrophil elastase. Other
 CC respiratory disorders such as cystic fibrosis are thought to be caused by
 CC human neutrophil elastase release by neutrophils. The genetically
 CC engineered human derived kunitz domains can be used to treat such
 CC respiratory disorders. See AAR92146-R9211. Fusion genes were used in the
 CC production of the kunitz domain derivatives. Protein expression cassettes
 CC are then cloned into the plasmid pHRV-D2 using BstBI and EcoRI
 CC restriction sites. The cloned sequence is under the transcriptional
 CC control of Pichia pastoris axi gene promoter and regulatory sequences
 CC and downstream polyadenylation and transcription termination sequences.
 CC Transformed strains of P. pastoris were used to express the various EPI-
 CC HNE proteins derived from the EPI and ITI-D2 kunitz domains. This
 CC sequence is a modified Kunitz domain (EPI-HNE-4) which was expressed from
 CC a pHRV-D2 plasmid construct
 XX
 SQ Sequence 141 AA;

Query Match 100.0%; Score 329; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 3.8e-34;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EACNLPYIRGPCIAPFPFMAFDVAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 56
 DB 86 EACNLPYIRGPCIAPFPFMAFDVAVKGCVLFPYGGCCGNGNKFYSEKREYCGVP 141

RESULT 6
 ABR84583
 ID ABR84583 standard; protein; 141 AA.
 XX
 AC ABR84583;
 XX
 DT 04-DEC-2003 (first entry)
 DE P pastoris prepro-EPI-HNE-4 mutated protein.
 XX
 KW EPI-hNE-4; EPI-HNE; alpha mating factor prepropeptide; mutant; mutagenic;
 KW mutein.
 XX
 OS Pichia pastoris.
 OS Synthetic.
 XX
 PN WO2003062431-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 23-JAN-2003; 2003WO-EP001212.
 XX
 PR 23-JAN-2002; 2002EP-00290166.
 XX
 PA (DEBI-) DEBIOPHARM SA.
 XX
 PI Gerard C, Poncin A, Saudubray F, Petchot-Bacque J;
 XX WPI: 2003-598755/56.
 DR N-PSDB; ACP04569.
 XX
 PT New fused gene constructs and expression vectors, useful for transforming
 PT microorganisms (particularly the yeast Pichia pastoris) for use in

PT producing e.g. EPI-hNE-4 proteins with very low levels of its improperly
PT processed form.

XX Example 2; Fig 1B; 27pp; English.

CC The present invention relates to a fused gene construct, which comprises
CC a nucleotide sequence coding for the *Saccharomyces cerevisiae* alpha
CC mating factor prepeptide or its variant, which is modified so as to
CC replace the lysine residue in position 76 of the amino acid sequence of
CC the naturally occurring prepeptide by an Alanine residue. The
CC nucleotide sequence is ligated to the 5' terminal of a nucleotide
CC sequence coding for EPI-hNE-4. An expression vector for the sequence is
CC also claimed. The gene construct or vector is useful for transforming
CC microorganisms (particularly yeast) to produce EPI-hNE-4 protein with
CC very low levels of its improperly processed form. The gene construct,
CC nucleotide sequence, expression vector or microorganism is useful for
CC producing or secreting a protein, particularly EPI-hNE-4, which contains
CC undetectable levels of the EPI-hNE-4 (n-9). This facilitates further
CC purification steps, and therefore results in economies both on the
CC financial and time-spent scale. The present sequence is a mutated version
CC of the *Pichia pastoris* EPI-hNE-4 protein used in the exemplification of
CC the invention

XX Sequence 141 AA;

Query Match 100.0%; Score 329; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPICIAFPFPMWDAVKGKCVLPYGGCGGNGKFKYSEKREYCGVP 56
DB 86 EACNLPYVGPICIAFPFPMWDAVKGKCVLPYGGCGGNGKFKYSEKREYCGVP 141

RESULT 7
ABR84585
ID ABR84585 standard; protein; 141 AA.

XX ABR84585;

XX 04-DEC-2003 (first entry)

XX Fusion sequence of alpha mating factor and EPI-hNE-4.

XX EPI-hNE-4; EPI-hNE; alpha mating factor prepeptide; fusion protein;
XX mutagenic.

XX *Saccharomyces cerevisiae*.

XX *Pichia pastoris*.

XX WO2003062431-A2.

XX 31-JUL-2003.

XX 23-JAN-2003; 2003WO-EP001212.

XX 23-JAN-2002; 2002EP-00290166.

XX (DEBI-) DEBIOPHARM SA.

XX Gerard C, Poncin A, Saudubray F, Petchot-Bacque J;

XX MPI; 2003-598755/56.

XX N-PSDB; ACP04571.

XX New fused gene constructs and expression vectors, useful for transforming
PT microorganisms (particularly the yeast *Pichia pastoris*) for use in
PT producing e.g. EPI-hNE-4 proteins with very low levels of its improperly
PT processed form.

XX Claim 4; Fig 10; 27pp; English.

XX The present invention relates to a fused gene construct, which comprises

CC a nucleotide sequence coding for the *Saccharomyces cerevisiae* alpha
CC mating factor prepeptide or its variant, which is modified so as to
CC replace the lysine residue in position 76 of the amino acid sequence of
CC the naturally occurring prepeptide by an Alanine residue. The
CC nucleotide sequence is ligated to the 5' terminal of a nucleotide
CC sequence coding for EPI-hNE-4. An expression vector for the sequence is
CC also claimed. The gene construct or vector is useful for transforming
CC microorganisms (particularly yeast) to produce EPI-hNE-4 protein with
CC very low levels of its improperly processed form. The gene construct,
CC nucleotide sequence, expression vector or microorganism is useful for
CC producing or secreting a protein, particularly EPI-hNE-4, which contains
CC undetectable levels of the EPI-hNE-4 (n-9). This facilitates further
CC purification steps, and therefore results in economies both on the
CC financial and time-spent scale. The present sequence is a fusion protein
CC containing the *S. cerevisiae* alpha mating factor prepeptide and the
CC *Pichia pastoris* EPI-hNE-4 protein used in the exemplification of the
CC invention

XX Sequence 141 AA;

Query Match 100.0%; Score 329; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPICIAFPFPMWDAVKGKCVLPYGGCGGNGKFKYSEKREYCGVP 56
DB 86 EACNLPYVGPICIAFPFPMWDAVKGKCVLPYGGCGGNGKFKYSEKREYCGVP 141

RESULT 8
ADF42042
ID ADF42042 standard; protein; 655 AA.

XX ADF42042;

XX 12-FEB-2004 (first entry)

XX N-terminal DX-890-(GGG) 4GG-albumin fusion protein.

XX albumin fusion; Kunitz domain; cytostatic; haemostatic;

XX hereditary angiodema; cancer; bleeding; gene therapy;

XX N-terminal DX-890-(GGG) 4GG-albumin fusion.

XX WO2003066824-A2.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003616.

XX 07-FEB-2002; 2002US-0355547P.

XX (AVENT) AVENTIS BEHRING GMBH.

XX (AVENT) AVENTIS BEHRING LLC.

XX (DELTA) DELTA BIOTECHNOLOGY LTD.

XX (DVAX-) DVAX CORP.

XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;

XX MPI; 2003-731497/69.

XX N-PSDB; ADF42041.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.

XX Example 23; Page 75; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its


```

ADR90034
ID   ADR90034 standard; protein; 655 AA.
XX
AC   ADR90034;
XX
DT   18-NOV-2004 (first entry)
XX
DE   N-terminal DX-890-(GGG)4 GG-albumin fusion protein.
XX
KW   Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW   hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW   asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW   cytosolic; haemostatic; chimeric; DX-890; human albumin; HA; human.
XX
OS   Homo sapiens.
OS   Chimeric.
OS   Unidentified.
XX
PN   US2004171794-A1.
XX
PD   02-SEP-2004.
XX
PF   07-FEB-2003; 2003US-00361997.
XX
PR   07-FEB-2003; 2003US-00361997.
XX
PA   (LADN/) LADNER R. C.
PA   (LEYA/) LEY A. C.
XX
PI   Ladner RC, Ley AC;
XX
DR   WPI; 2004-625120/60.
DR   N-PSDB; ADR90033.
XX
PT   New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT   for the treatment of e.g. cystic fibrosis and related disease.
XX
PS   Example 8; SEQ ID NO 59; 123bp; English.
XX
CC   The invention relates to proteins comprising kunitz domain peptide,
CC   designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC   albumin. The invention is useful for treating cystic fibrosis and related
CC   diseases, hereditary angioedema, cancer and related diseases including
CC   chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC   respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC   cytosolic and haemostatic agent. The present sequence is a N-terminal DX
CC   -890-(GGG)4 GG-albumin fusion protein. This fusion protein contains DX-
CC   890 cDNA encoding protein, GS linker region and human albumin (HA)
CC   encoding protein. This sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 655 AA;

Query Match          100.0%; Score 329; DB 8; Length 655;
Best Local Similarity 100.0%; Pred. No. 2,1e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 EACNLPYVGGPCIAFPFPRWAFDAVKKCVLPFYGGCGGNGKFFYSEKCREYCGVP 56
    1 EACNLPYVGGPCIAFPFPRWAFDAVKKCVLPFYGGCGGNGKFFYSEKCREYCGVP 56
DB   1 EACNLPYVGGPCIAFPFPRWAFDAVKKCVLPFYGGCGGNGKFFYSEKCREYCGVP 56

RESULT 12
ADR42054
ID   ADR42054 standard; protein; 694 AA.
XX
AC   ADR42054;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Plasmid pDB2300X2 NotI modified expression cassette protein.
XX
KW   albumin fusion; Kunitz domain; cytosolic; haemostatic;

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```

KW   hereditary angioedema; cancer; bleeding; gene therapy;
KW   plasmid pDB2300X2 NotI expression cassette; DX-890.
XX
OS   Synthetic.
OS   Unidentified.
XX
PN   WO2003066824-A2.
XX
PD   14-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003616.
XX
PR   07-FEB-2002; 2002US-0355547P.
XX
PA   (AVET ) AVENTIS BEHRING GMBH.
PA   (AVET ) AVENTIS BEHRING LLC.
PA   (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA   (DYAX-) DYAX CORP.
XX
PI   Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
PI   Ley AC;
XX
DR   WPI; 2003-731497/69.
DR   N-PSDB; ADF42053.
XX
PT   Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT   useful for preparing a composition for treating a patient with hereditary
PT   angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
PS   Example 23; Page 85-89; 110bp; English.
XX
CC   The invention relates to a novel albumin fusion protein comprising a
CC   Kunitz domain peptide or its fragment or variant and an albumin or its
CC   fragment or variant. The fusion protein of the invention demonstrates
CC   cytosolic and haemostatic activities and may be useful for preparing a
CC   composition for treating a patient with hereditary angioedema, an
CC   angioedema-related disease, cancer, a cancer-related disease or a
CC   bleeding disorder, as well as during gene therapy procedures. The current
CC   sequence is that of the albumin fusion protein-related plasmid pDB2300X2
CC   modified NotI expression cassette protein of the invention which has N-
CC   terminal DX-890 and C-terminal linker ready for a second DX-890 sequence.
XX
SQ   Sequence 694 AA;

Query Match          100.0%; Score 329; DB 7; Length 694;
Best Local Similarity 100.0%; Pred. No. 2,2e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 EACNLPYVGGPCIAFPFPRWAFDAVKKCVLPFYGGCGGNGKFFYSEKCREYCGVP 56
    1 EACNLPYVGGPCIAFPFPRWAFDAVKKCVLPFYGGCGGNGKFFYSEKCREYCGVP 56
DB   25 EACNLPYVGGPCIAFPFPRWAFDAVKKCVLPFYGGCGGNGKFFYSEKCREYCGVP 80

RESULT 13
ADR90046
ID   ADR90046 standard; protein; 694 AA.
XX
AC   ADR90046;
XX
DT   18-NOV-2004 (first entry)
XX
DE   pDB2300X2-2xGS linker fusion protein.
XX
KW   Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW   hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW   asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW   cytosolic; haemostatic; chimeric; human; rHA synthase gene;
KW   human albumin; HA.
XX
OS   Homo sapiens.
OS   Chimeric.
OS   Unidentified.

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FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein /label= Signal_peptide
FT Region 25..694
FT Region /note= "Mature pDB2300X2-2xGS linker fusion protein"
FT Region 25..80
FT Region /note= "DX-890 protein"
FT Region 81..94
FT Region /note= "GS-linker region"
FT Region 95..679
FT Region /note= "rHA protein"
PN US2004171794-A1.
XX
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX (LADN/) LADNER R C.
XX (LEYA/) LEY A C.
XX
XX Ladhner RC, Ley AC;
XX
XX MPI: 2004-625120/60.
XX DR N-FSDB; ADR90045.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX PT for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Example 18; SEQ ID NO 71; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
XX CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX CC albumin. The invention is useful for treating cystic fibrosis and related
XX CC diseases, hereditary angioedema, cancer and related diseases including
XX CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX CC cyostatic and haemostatic agent. The present sequence is a pDB2300X2-
XX CC 2xGS linker fusion protein. This chimeric protein contains DX-890 protein
XX CC at its N-terminal end, rHA synthase gene encoding protein and linkers at
XX CC its C-terminal end. This sequence is used in the exemplification of the
XX CC invention.
XX
XX SQ Sequence 694 AA;
XX
XX Query Match 100.0%; Score 329; DB 8; Length 694;
XX Best Local Similarity 100.0%; Pred. No. 2,2e-33;
XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EACNLPYRGPCIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFFYSEKREYCGVP 56
XX |||||
XX DB 25 EACNLPYRGPCIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFFYSEKREYCGVP 80
XX |||||
XX
XX RESULT 14
XX ADF42058
XX ID ADF42058 standard; protein; 728 AA.
XX
XX AC ADF42058;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Albumin fusion-related DX-890. (GGS) 4GG. HA. (GGS) 4GG. DX-890 protein.
XX
XX KW albumin fusion; kunitz domain; cyostatic; haemostatic;
XX KW hereditary angioedema; cancer; bleeding; gene therapy; (GGS) 4GG; DX-890;
XX HA.
XX
XX OS Synthetic.
XX OS Unidentified.
XX

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PN WO2003066824-A2.
XX
XX 14-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003616.
XX
XX 07-FEB-2002; 2002US-0355547P.
XX
XX (AVET ) AVENTIS BEHRING GMBH.
XX PA (AVET ) AVENTIS BEHRING LLC.
XX PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
XX PA (DYAX-) DYAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladhner RC;
XX PI Ley AC;
XX
XX MPI: 2003-731497/69.
XX
XX Albumin fusion protein comprising a kunitz domain peptide and an albumin,
XX PT useful for preparing a composition for treating a patient with hereditary
XX PT angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
XX Example 23; Page 94-95; 110pp; English.
XX
XX The invention relates to a novel albumin fusion protein comprising a
XX CC kunitz domain peptide or its fragment or variant and an albumin or its
XX CC fragment or variant. The fusion protein of the invention demonstrates
XX CC cyostatic and haemostatic activities and may be useful for preparing a
XX CC composition for treating a patient with hereditary angioedema, an
XX CC angioedema-related disease, cancer, a cancer-related disease or a
XX CC bleeding disorder, as well as during gene therapy procedures. The current
XX CC sequence is that of the albumin fusion protein-related DX-
XX CC 890. (GGS) 4GG. HA. (GGS) 4GG. DX-890 protein of the invention.
XX
XX SQ Sequence 728 AA;
XX
XX Query Match 100.0%; Score 329; DB 7; Length 728;
XX Best Local Similarity 100.0%; Pred. No. 2,3e-33;
XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EACNLPYRGPCIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFFYSEKREYCGVP 56
XX |||||
XX DB 1 EACNLPYRGPCIAFPFRWAFDAVKGKCVLPFYGGCGGNGKFFYSEKREYCGVP 56
XX |||||
XX
XX RESULT 15
XX ADR90050
XX ID ADR90050 standard; protein; 728 AA.
XX
XX AC ADR90050;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Mature pDB2300X3-2xDX-890 fusion protein.
XX
XX KW kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
XX KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
XX KW cyostatic; haemostatic; chimeric; human; rHA synthase gene;
XX KW human albumin; HA; DX-890.
XX
XX OS Homo sapiens.
XX OS Chimeric.
XX OS Unidentified.
XX
XX PN US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX

```

PA (LADN/) LADNER R C.
PA (LEYA/) LEY A C.
XX
XX
PI Lader RC, Ley AC;
XX
XX WPI; 2004-625120/60.
DR N-PSDB; ADR90048.
XX
PT New knitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
XX
XX Example 19; SEQ ID NO 75; 123pp; English.
XX
XX The invention relates to proteins comprising knitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytoskeletal and haemostatic agent. The present sequence is a mature
CC PDB3100X3-2XDX-890 fusion protein. This chimeric protein contains two DX-
CC 890 proteins, rHA synthase gene encoding protein and the linkers. This
CC sequence is used in the exemplification of the invention.
XX
SQ Sequence 728 AA;
XX
Query Match 100.0%; Score 329; DB 8; Length 728;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
DB 1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
XX
RESULT 16
ADFA42029
ID ADFA42029 standard; protein; 729 AA.
XX
XX ADFA42029;
AC
XX 12-FEB-2004 (first entry)
DT
XX
XX DPI-14- (GGS) 4GG-rHA- (GGS) 4GG-DX-890 fusion mature protein.
DE
XX
XX albumin fusion; knitz domain; cytoskeletal; haemostatic;
XX hereditary angioedema; cancer; bleeding; gene therapy; plasmid PDB310X;
KM DPI-14- (GGS) 4GG-rHA- (GGS) 4GG-DX-890 fusion; mature.
XX
XX Synthetic.
OS
XX Undifferentiated.
OS
XX WO2003066824-A2.
PN
XX 14-AUG-2003.
PD
XX
XX 07-FEB-2003; 2003WO-US003616.
PF
XX
XX 07-FEB-2002; 2002US-0355547P.
PR
XX
XX (AVENT) AVENTIS BEHRING GMBH.
PA (AVENT) AVENTIS BEHRING LLC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (DYAX-) DYAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Lader RC,
PI Ley AC;
XX
XX WPI; 2003-731497/69.
DR
XX
XX Albumin fusion protein comprising a knitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.

XX
XX Example 22; Page 68-69; 110pp; English.
PS
XX
XX The invention relates to a novel albumin fusion protein comprising a
CC knitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates
CC cytoskeletal and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the plasmid PDB310X-derived DPI-14- (GGS) 4GG-rHA-
CC (GGS) 4GG-DX-890 fusion mature protein of the invention.
XX
SQ Sequence 729 AA;
XX
Query Match 100.0%; Score 329; DB 7; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
1 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 56
DB 674 EACNLPYVRGPCIAPFPFMAFDVAVKGCVLFPYGGCGGNGKPFYSEKREYCGVP 729
XX
RESULT 17
ADR90021
ID ADR90021 standard; protein; 729 AA.
XX
XX ADR90021;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Mature DPI-14- (GGS) 4 GG-rHA- (GGS) 4 GG-DX-890 fusion protein.
DE
XX
XX Knitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;
XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KM cytoskeletal; haemostatic; human; rHA synthase gene; human albumin; HA;
XX DPI-14; DX-890; chimeric.
XX
XX Homo sapiens.
OS
XX Chimeric.
OS
XX Undifferentiated.
OS
XX US2004171794-A1.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 07-FEB-2003; 2003US-00361997.
PF
XX
XX 07-FEB-2003; 2003US-00361997.
PR
XX
XX (LADN/) LADNER R C.
PA (LEYA/) LEY A C.
PA
XX
XX Lader RC, Ley AC;
PI
XX
XX WPI; 2004-625120/60.
DR
XX
XX N-PSDB; ADR90019.
DR
XX
XX New knitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
PT
XX
XX Example 22; SEQ ID NO 46; 123pp; English.
PS
XX
XX The invention relates to proteins comprising knitz domain peptide,
CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
CC albumin. The invention is useful for treating cystic fibrosis and related
CC diseases, hereditary angioedema, cancer and related diseases including
CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
CC cytoskeletal and haemostatic agent. The present sequence is a mature DPI-14
CC - (GGS) 4 GG-rHA- (GGS) 4 GG-DX-890 fusion protein. This fusion protein

CC contains DPI-14 cDNA encoding protein, GS linker region, rHA (human
CC albumin) synthase gene encoding protein and DX-890 encoding protein. This
CC sequence is used in the exemplification of the invention.

XX Sequence 729 AA;

Query Match 100.0%; Score 329; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
674 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 729

RESULT 18

ADP42057
ID ADP42057 standard; protein; 752 AA.

XX ADP42057;

XX 12-FEB-2004 (first entry)

XX Plasmid PDB2300X3 NotI modified expression cassette protein - 2X DX-890.

XX albumin fusion; Kunitz domain; cytostratic; haemostatic;

XX hereditary angioedema; cancer; bleeding; gene therapy;

XX plasmid PDB2300X3 NotI expression cassette; DX-890..

XX Synthetic.

XX Unidentified.

XX WO2003066824-A2.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003616.

XX 07-FEB-2002; 2002US-0355547P.

XX (AVET) AVENTIS BEHRING GMBH.

XX (AVET) AVENTIS BEHRING LLC.

XX (DELZ) DELTA BIOTECHNOLOGY LTD.

XX (DYAX-) DYAX CORP.

XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;

XX Ley AC;

XX WPI; 2003-731497/69.

XX N-PSDB; ADP42056.

XX The invention relates to a novel albumin fusion protein comprising a

XX Kunitz domain peptide or its fragment or variant and an albumin or its

XX fragment or variant. The fusion protein of the invention demonstrates

XX cytostratic and haemostatic activities and may be useful for preparing a

XX composition for treating a patient with hereditary angioedema, an

XX angioedema-related disease, cancer, a cancer-related disease or a

XX bleeding disorder, as well as during gene therapy procedures. The current

XX sequence is that of the albumin fusion protein-related plasmid PDB2300X3

XX modified NotI expression cassette protein of the invention which has 2 DX

XX -890 sequences.

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
25 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 80

Query Match 100.0%; Score 329; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
674 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 729

RESULT 19

ADR90049
ID ADR90049 standard; protein; 752 AA.

XX ADR90049;

XX 18-NOV-2004 (first entry)

XX PDB2300X3-2XDX-890 fusion protein.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;

XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

XX cytostratic; haemostatic; chimeric; human; rHA synthase gene;

XX human albumin; HA; DX-890.

XX Homo sapiens.

XX Chimeric.

XX Unidentified.

XX Key

XX Peptide

XX Protein

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

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XX Region

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
25 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 80

Query Match 100.0%; Score 329; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
674 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 729

RESULT 19

ADR90049
ID ADR90049 standard; protein; 752 AA.

XX ADR90049;

XX 18-NOV-2004 (first entry)

XX PDB2300X3-2XDX-890 fusion protein.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;

XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

XX cytostratic; haemostatic; chimeric; human; rHA synthase gene;

XX human albumin; HA; DX-890.

XX Homo sapiens.

XX Chimeric.

XX Unidentified.

XX Key

XX Peptide

XX Protein

XX Region

XX Region

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1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
25 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 80

Query Match 100.0%; Score 329; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
674 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 729

RESULT 19

ADR90049
ID ADR90049 standard; protein; 752 AA.

XX ADR90049;

XX 18-NOV-2004 (first entry)

XX PDB2300X3-2XDX-890 fusion protein.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;

XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

XX cytostratic; haemostatic; chimeric; human; rHA synthase gene;

XX human albumin; HA; DX-890.

XX Homo sapiens.

XX Chimeric.

XX Unidentified.

XX Key

XX Peptide

XX Protein

XX Region

XX Region

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1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
25 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 80

Query Match 100.0%; Score 329; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
674 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 729

RESULT 19

ADR90049
ID ADR90049 standard; protein; 752 AA.

XX ADR90049;

XX 18-NOV-2004 (first entry)

XX PDB2300X3-2XDX-890 fusion protein.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;

XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

XX cytostratic; haemostatic; chimeric; human; rHA synthase gene;

XX human albumin; HA; DX-890.

XX Homo sapiens.

XX Chimeric.

XX Unidentified.

XX Key

XX Peptide

XX Protein

XX Region

XX Region

XX Region

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1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
25 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 80

Query Match 100.0%; Score 329; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
674 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 729

RESULT 19

ADR90049
ID ADR90049 standard; protein; 752 AA.

XX ADR90049;

XX 18-NOV-2004 (first entry)

XX PDB2300X3-2XDX-890 fusion protein.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;

XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

XX cytostratic; haemostatic; chimeric; human; rHA synthase gene;

XX human albumin; HA; DX-890.

XX Homo sapiens.

XX Chimeric.

XX Unidentified.

XX Key

XX Peptide

XX Protein

XX Region

XX Region

XX Region

XX Region

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1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
25 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 80

Query Match 100.0%; Score 329; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 56
674 EACNLPIVRGPCIAFFPRMAFDVAKGKCVLPFYGGCGGNGNKFYSEKREYCGVP 729

RESULT 19

ADR90049
ID ADR90049 standard; protein; 752 AA.

XX ADR90049;

XX 18-NOV-2004 (first entry)

XX PDB2300X3-2XDX-890 fusion protein.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;

XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

XX cytostratic; haemostatic; chimeric; human; rHA synthase gene;

XX human albumin; HA; DX-890.

XX Homo sapiens.

XX Chimeric.

XX Unidentified.

XX Key

XX Peptide

XX Protein

XX Region

XX Region

XX Region

XX Region

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XX Region

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XX
SQ Sequence 752 AA;

Query Match 100.0%; Score 329; DB 8; Length 752;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EACNLPYVGPCTIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSKREYCGVP 56
DB 25 EACNLPYVGPCTIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSKREYCGVP 80

RESULT 20
ADFA42028
ID ADFA42028 standard; protein; 753 AA.

AC ADFA42028;

DT 12-FEB-2004 (first entry)

DE DPI-14- (GGS) 4GG-rHA- (GGS) 4GG-DX-890 fusion precursor protein.

XX albumin fusion; Kunitz domain; cytosolic; haemostatic;
KW hereditary angioedema; cancer; bleeding; gene therapy; plasmid pDB2301X;
KM DPI-14- (GGS) 4GG-rHA- (GGS) 4GG-DX-890 fusion; precursor.

XX Synthetic.
OS Unidentified.

PN WO2003066824-A2.

PD 14-AUG-2003.

PF 07-FEB-2003; 2003WO-US003616.

PR 07-FEB-2002; 2002US-0355547P.

PA (AVET) AVENTIS BEHRING GMBH.

PA (AVET) AVENTIS BEHRING LLC.

PA (DELZ) DELTA BIOTECHNOLOGY LTD.

PA (DYAX-) DYAX CORP.

PI Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;

PI Ley AC;

XX MPI: 2003-731497/69.

DR N-PSDB; ADFA42068.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,

PT useful for preparing a composition for treating a patient with hereditary

PT angioedema or angioedema-related disease, cancer or bleeding disorder.

PS Example 22; Page 68; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a

CC Kunitz domain peptide or its fragment or variant and an albumin or its

CC fragment or variant. The fusion protein of the invention demonstrates

CC cytosolic and haemostatic activities and may be useful for preparing a

CC composition for treating a patient with hereditary angioedema, an

CC angioedema-related disease, cancer, a cancer-related disease or a

CC bleeding disorder, as well as during gene therapy procedures. The current

CC sequence is that of the plasmid pDB2301X-derived DPI-14- (GGS) 4GG-rHA-

CC (GGS) 4GG-DX-890 fusion precursor protein of the invention.

XX Sequence 753 AA;

QY Query Match 100.0%; Score 329; DB 7; Length 753;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 EACNLPYVGPCTIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSKREYCGVP 56
698 EACNLPYVGPCTIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSKREYCGVP 753

RESULT 21

ADR90020

ADFA42028

ADFA42028 standard; protein; 753 AA.

AC ADFA42028;

DT 18-NOV-2004 (first entry)

DE DPI-14- (GGS) 4 GG-rHA- (GGS) 4 GG-DX-890 fusion protein.

XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;

KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;

KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;

KW cytosolic; haemostatic; human; rHA synthase gene; human albumin; HA;

KW DPI-14; DX-890; chimeric.

OS Homo sapiens.

OS Chimeric.

OS Unidentified.

PN US2004171794-A1.

PD 02-SEP-2004.

PF 07-FEB-2003; 2003US-00361997.

PR 07-FEB-2003; 2003US-00361997.

PA (LADN/) LADNER R C.

PA (LEVA/) LEY A C.

PI Ladner RC, Ley AC;

XX MPI: 2004-625120/60.

DR N-PSDB; ADR90019.

XX New Kunitz domain peptide useful as human neutrophil elastase inhibitor

PT for the treatment of e.g. cystic fibrosis and related disease.

PS Example 22; SEQ ID NO 45; 123pp; English.

XX The invention relates to proteins comprising Kunitz domain peptide,

CC designated DPI-14 for inhibiting human neutrophil elastase, fused to

CC albumin. The invention is useful for treating cystic fibrosis and related

CC diseases, hereditary angioedema, cancer and related diseases including

CC chronic obstructive pulmonary disease, asthma, bronchitis, acute

CC respiratory syndrome, pneumonia and bleeding. The invention acts as a

CC cytosolic and haemostatic agent. The present sequence is a DPI-14- (GGS) 4

CC GG-rHA- (GGS) 4 GG-DX-890 fusion protein. This fusion protein contains DPI-

CC 14 CDNA encoding protein, GS linker region, rHA (human albumin) synthase

CC gene encoding protein and DX-890 encoding protein. This sequence is used

CC in the exemplification of the invention.

XX Sequence 753 AA;

QY Query Match 100.0%; Score 329; DB 8; Length 753;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 EACNLPYVGPCTIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSKREYCGVP 56
698 EACNLPYVGPCTIAFFPRMAFDVAVKGCVLFPYGGCGGNGNKFYSKREYCGVP 753

RESULT 22
AAR99167
ID AAR99167 standard; protein; 56 AA.

AC AAR99167;

DT 12-FEB-1997 (first entry)

XX Genetically engineered aprotinin-like Kunitz domain (BPI-HNE-3).
DE Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
XX connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
XX smokers emphysema.
XX Synthetic.
OS
XX WO9620278-A2.
PN
XX 04-JUL-1996.
PD
XX 15-DEC-1995; 95WO-US016349.
PF
XX 16-DEC-1994; 94US-00358160.
PR
XX (PROT-) PROTEIN ENG CORP.
PA
XX Ley AC, Ladner RC, Guerman SK, Roberts BL, Markland W, Kent RB;
PI WPI; 1996-321851/32.
DR
XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
XX Claim 1; Page 49; 105pp; English.
PS
XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha1
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR9146-R99211
XX
SQ Sequence 56 AA;
Query Match 98.5%; Score 324; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 6.2e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 ACNLPYVAGPCIAFPFPMWFDVAVKGVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 2 ACNLPYVAGPCIAFPFPMWFDVAVKGVLPFYGGCGGNGNKFYSKEKREYCGVP 56
RESULT 23
ADF71967
ID ADF71967 standard; protein; 56 AA.
AC ADF71967;
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Kallikrein inhibitor related amino acid sequence SEQ ID NO:47.
DE
XX ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
KW systemic inflammatory response.
XX
XX Homo sapiens.
OS
XX WO2003103475-A2.
PN
XX 18-DEC-2003.
PD
XX 06-JUN-2003; 2003WO-US017665.
PF

XX 07-JUN-2002; 2002US-0387239P.
PR 28-AUG-2002; 2002US-0407003P.
XX
XX (DYAX-) DYAX CORP.
PA
XX
XX Ladner RC, Ley AC, Hiranani S, Williams A;
PI WPI; 2004-062190/06.
DR
XX
XX Preventing or reducing ischemia in patient involves administering to
PT patient composition comprising a kallikrein inhibitory polypeptide.
PT
XX
XX Disclosure; SEQ ID NO 47; 46pp; English.
PS
XX The present invention describes a method (M1) for preventing or reducing
CC ischaemia in a patient. M1 involves administering to the patient a
CC composition comprising a polypeptide (I) having an amino acid sequence of
CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can
CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
CC reducing ischaemia in a patient such as peroperative blood loss due to a
CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
CC is also useful for preventing or reducing the onset of systemic
CC inflammatory response associated with a surgical procedure in a patient
CC which involves administering (I) to a patient. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 56 AA;
Query Match 98.5%; Score 324; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 6.2e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 ACNLPYVAGPCIAFPFPMWFDVAVKGVLPFYGGCGGNGNKFYSKEKREYCGVP 56
Db 2 ACNLPYVAGPCIAFPFPMWFDVAVKGVLPFYGGCGGNGNKFYSKEKREYCGVP 56
RESULT 24
ADF71968
ID ADF71968 standard; protein; 56 AA.
AC ADF71968;
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Kallikrein inhibitor related amino acid sequence SEQ ID NO:48.
DE
XX ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
KW systemic inflammatory response.
XX
XX Homo sapiens.
OS
XX WO2003103475-A2.
PN
XX 18-DEC-2003.
PD
XX 06-JUN-2003; 2003WO-US017665.
PF
XX 07-JUN-2002; 2002US-0387239P.
PR 28-AUG-2002; 2002US-0407003P.
XX
XX (DYAX-) DYAX CORP.
PA
XX
XX Ladner RC, Ley AC, Hiranani S, Williams A;
PI WPI; 2004-062190/06.
DR
XX
XX Preventing or reducing ischemia in patient involves administering to
PT patient composition comprising a kallikrein inhibitory polypeptide.
PT
XX
XX Disclosure; SEQ ID NO 48; 46pp; English.
PS

XX The present invention describes a method (M1) for preventing or reducing
 CC ischaemia in a patient. M1 involves administering to the patient a
 CC composition comprising a polypeptide (I) having an amino acid sequence of
 CC ADP1926 and inhibiting kallikrein. (I) has vasotropic activity, and can
 CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
 CC reducing ischaemia in a patient such as peroperative blood loss due to a
 CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
 CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
 CC is also useful for preventing or reducing the onset of systemic
 CC inflammatory response associated with a surgical procedure in a patient
 CC which involves administering (I) to a patient. The present sequence is
 CC used in the exemplification of the present invention.

XX Sequence 56 AA;

Query Match 98.5%; Score 324; DB 8; Length 56;
 Best Local Similarity 100.0%; Pred. No. 6.2e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ACNLPYVRGPCIAPFPFWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
 DB 2 ACNLPYVRGPCIAPFPFWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56

RESULT 25

AAR9214
 ID AAR9214 standard; protein; 141 AA.

AC AAR9214;

DT 14-FEB-1997 (first entry)

DE Modified Kunitz domain EPI-HNE-3.

KW Agprotinin; Kunitz domain; human neutrophil elastase; hNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alaph antitrypsin; respiratory disorder; cystic fibrosis;
 KW smokers emphysema.

OS Synthetic.

PN WO9620278-A2.

PD 04-JUL-1996.

PF 15-DEC-1995; 95WO-US016349.

PR 16-DEC-1994; 94US-00358160.

PA (PROT-) PROTEIN ENG CORP.

PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

DR WPI; 1996-321851/32.

DR N-PSDB; AAT35166, AAT35168.

PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin
 PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
 PT respiratory disorders.

PS Claim 1; Page 68-69; 105pp; English.

XX Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the elimination
 CC of pathogens and the restructuring of connective tissue. In cases of
 CC reduction of the circulating alpha-1-protease inhibitor (API or alaph
 CC antitrypsin), or the inactivation of API by oxidation (smokers
 CC emphysema), extensive destruction of the lung tissue may result from
 CC uncontrolled elastolytic activity of human neutrophil elastase. Other
 CC respiratory disorders such as cystic fibrosis are thought to be caused by
 CC human neutrophil elastase release by neutrophils. The genetically
 CC engineered human derived Kunitz domains can be used to treat such

CC respiratory disorders. See AAR92146-R9211. Fusion genes were used in the
 CC production of the Kunitz domain derivatives. Protein expression cassettes
 CC are then cloned into the plasmid pHLI-D2 using BstBI and EcoRI
 CC restriction sites. The cloned sequence is under the transcriptional
 CC control of pichia pastoris axol gene promoter and regulatory sequences
 CC and downstream polyadenylation and transcription termination sequences.
 CC Transformed strains of P. pastoris were used to express the various EPI-
 CC HNE proteins derived from the BPTI and ITI-D2 Kunitz domains. This
 CC sequence is a modified Kunitz domain (EPI-HNE-3) which was expressed from
 CC a pHLI-D2 plasmid construct designated pHLI-D2 (Mfalp)apPrePro-EPI-HNE-3)

XX Sequence 141 AA;

Query Match 98.5%; Score 324; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ACNLPYVRGPCIAPFPFWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 56
 DB 87 ACNLPYVRGPCIAPFPFWAFDAVKGKCVLPFYGGCGGNGNKFYSKEKREYCGVP 141

Search completed: February 23, 2005, 03:28:14
 Job time : 75 secs